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OM protein - protein search, using sw model

Run on: January 28, 2003, 09:22:43 ; Search time 39 seconds
(without alignments)
2244.760 Million cell updates/sec

Title: US-09-863-818a-12
Perfect score: 3512
Sequence: 1 MGSSRLAALLPLLLIVIDL.....SRLECSRLERARLADLG 657

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002:*

1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*

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4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*

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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3512	100.0	657	23	AAU11356 Human DNAX cytokin
2	2711	77.2	667	22	AAU04957 Human Interleukin
3	2711	77.2	667	23	AAU83601 Human PRO protein,
4	1831.5	52.1	617	21	AAU76048 Murine skin cell p
5	1831.5	52.1	617	22	AAU55987 Skin cell protein,
6	1831.5	52.1	617	23	AAU72187 Murine protein iso
7	1108	31.5	226	23	AAU83238 Novel secreted pro
8	948.5	27.0	330	21	AAU75947 Murine skin cell s
9	948.5	27.0	330	22	AAU55886 Skin cell protein,
10	948.5	27.0	330	23	AAU72086 Murine protein iso

11	547	15.6	353	22	ABG08185	Novel human diapo
12	438	12.5	145	22	ABG08183	Novel human diapo
13	435.5	12.4	243	23	AAU11357	Mouse DNAX cytokin
14	318	9.1	698	23	ABU72297	Murine protein iso
15	318	9.1	698	23	AAU11354	Mouse DNAX cytokin
16	313	8.9	698	23	AAE14560	Murine cytokine re
17	312.5	8.9	674	23	AAE14559	Murine cytokine re
18	311	8.9	720	23	AAU98781	Human full length
19	309	8.8	698	23	AAU99161	Mouse interleukin
20	304.5	8.7	692	22	AAU61880	Human cytokine rec
21	304.5	8.7	692	23	AAE14562	Human cytokine rec
22	300	8.5	705	23	AAU98792	Human interleukin
23	299	8.5	705	22	AAU29322	Human PRO polypept
24	299	8.5	705	22	AAU04956	Human Interleukin
25	299	8.5	705	22	AAU61884	Human PRO20040 H
26	299	8.5	705	22	AAU61884	Chimeric zcytor14
27	299	8.5	705	23	ABU5604	Human angiotensin
28	299	8.5	705	23	ABU84998	Human PRO20040 pro
29	292	8.3	683	23	AAU98789	Human Interleukin
30	288	8.2	703	23	AAU98791	Human Interleukin
31	284	8.1	675	22	AAU61885	Chimeric zcytor14
32	281	8.0	703	23	AAU11353	Human DNAX cytokin
33	278.5	7.9	688	22	AAU61883	Chimeric zcytor14
34	274.5	7.8	187	22	AAU23494	Human EST encoded
35	274	7.8	575	22	AAU61881	Human variant zcyt
36	248	7.1	693	23	AAU98790	Human Interleukin
37	173	4.9	553	23	AAU98788	Human Interleukin
38	155.5	4.4	409	23	AAU98787	Human Interleukin
39	153	4.4	204	22	AAE10920	Human gene 12 enco
40	137.5	3.9	539	23	AAU47457	Human IL-17 recept
41	136	3.9	372	23	AAU98786	Human Interleukin
42	134	3.8	348	23	AAU98785	Human Interleukin
43	123	3.5	866	17	AAU04185	Human Interleukin
44	123	3.5	866	19	AAU61272	Human Interleukin
45	123	3.5	866	20	AAU92409	Human IL-17 prote

ALIGNMENTS

RESULT 1
AAU11356
ID AAU11356 standard; Protein; 657 AA.
XX
AC AAU11356;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX cytokine receptor subunit 9 (DCRS9) polypeptide.
DE
DE Human; DNAX cytokine receptor subunit 9; DCRS9; phosphate labelling;
KW gene therapy; protein therapy; immunological disorder.
XX
OS Homo sapiens.
XX
PN WO200190358-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US16767.
PR 24-MAY-2000; 2000US-206862P.
XX
XX (SCHE) SCHERING CORP.
XX
XX Gorman DM;
XX
XX WPI; 2002-106198/14.
XX
XX N-PSDB; AAS18136.
XX
XX Isolated antigenic human or mouse DNAX receptor subunit-like
XX polypeptide useful for detecting antibodies generated in response to
XX presence of increased protein levels or immunological disorders -

XX PS Claim 1: page 29; 148pp; English.

XX CC The invention relates to primate and rodent DNAX cytokine receptor

CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The

CC receptors, or their portions may be useful as phosphate labelling enzymes

CC to label general or specific substrates. The subunits may also be

CC functional immunogens to elicit recognising antibodies, or antigens

CC capable of binding antibodies. A combination, e.g., including a DCRS can

CC be used as an immunogen for the production of antisera or antibodies

CC capable of distinguishing between other cytokine receptor family members.

CC A purified DCRS can also be used as a reagent to detect antibodies

CC generated in response to the presence of elevated levels of expression,

CC or immunological disorders which lead to antibody production to the

CC endogenous receptor. This sequence represents the human DCRS9

CC polypeptide.

XX SQ Sequence 657 AA:

Query Match 100.0%; Score 3512; DB 23; Length 657;

Best Local Similarity 100.0%; Pred. No. 6.8e-313;

Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSSRLAALLPLLIVIDLSDSAGTGFRRHLPWNTRCPLASHTVLPISLAAPGGPSP 60

Db 1 MGSSRLAALLPLLIVIDLSDSAGTGFRRHLPWNTRCPLASHTVLPISLAAPGGPSP 60

QY 61 QSLGVCESTVPACASICQVAVNGASSTWCNRPKSLPHSSSIGDTRCQHLLRGSC 120

Db 61 QSLGVCESTVPACASICQVAVNGASSTWCNRPKSLPHSSSIGDTRCQHLLRGSC 120

QY 121 CLVVTCLRRRAITPPSPQTSPTDFALKGNLRIQRHGKVFDPWTHKMEVGTGYNRRW 180

Db 121 CLVVTCLRRRAITPPSPQTSPTDFALKGNLRIQRHGKVFDPWTHKMEVGTGYNRRW 180

QY 181 QLSGGPEFSDLLPEARIVRTISSGPEVSVRLCHOWALECELSPPDYQKIVSGGHV 240

Db 181 QLSGGPEFSDLLPEARIVRTISSGPEVSVRLCHOWALECELSPPDYQKIVSGGHV 240

QY 241 ELPEYFLLPCLCEASYLQEDTVRRKKCPQSWPEAYGSDFWKSVHFTDY SHTQVMVAL 300

Db 241 ELPEYFLLPCLCEASYLQEDTVRRKKCPQSWPEAYGSDFWKSVHFTDY SHTQVMVAL 300

QY 301 TLRCPKLEAALCORHDMHTLCKDLPNATARES DGNVYVLEKVDLHPQLCFKVPWFSEFN 360

Db 301 TLRCPKLEAALCORHDMHTLCKDLPNATARES DGNVYVLEKVDLHPQLCFKVPWFSEFN 360

QY 361 SSHVECPHOTGSLTSWNVSMDTQAQQLILHFSRMMHATFSAAWSLPCLGODTLVPPVTV 420

Db 361 SSHVECPHOTGSLTSWNVSMDTQAQQLILHFSRMMHATFSAAWSLPCLGODTLVPPVTV 420

QY 421 SQVRSVDQFAWKHLCPDYSYRHLGLLILALLALLTLGLVVALTCRRPQSGPGPARPV 480

Db 421 SQVRSVDQFAWKHLCPDYSYRHLGLLILALLALLTLGLVVALTCRRPQSGPGPARPV 480

QY 481 LLLHAADSEAOQRLVGVGALAEALLRAALGGGRDVIIDLMEGRHVARVGPLPWLWAARTVAR 540

Db 481 LLLHAADSEAOQRLVGVGALAEALLRAALGGGRDVIIDLMEGRHVARVGPLPWLWAARTVAR 540

QY 541 EQGVTLVLSGADLRPVGGPDPAAPLILHHAAPRPLLLAYFSRLCAKGDIPPLRAL 600

Db 541 EQGVTLVLSGADLRPVGGPDPAAPLILHHAAPRPLLLAYFSRLCAKGDIPPLRAL 600

QY 601 PRYRLRLDPLRLRALDARPAEATSWGRLGARQRRQSRLELCSRLEREAAARLADLG 657

Db 601 PRYRLRLDPLRLRALDARPAEATSWGRLGARQRRQSRLELCSRLEREAAARLADLG 657

RESULT 2

AAU04957

ID AAU04957 standard; Protein: 667 AA.

XX AC AAU04957;

XX 24-OCT-2001 (first entry)

DT Human Interleukin 17 receptor, IL-17RH3.

DE

XX Human; Interleukin-17 receptor; IL-17RH3; agonist; antagonist;

KW PR09877; DNA I19502-2789; systemic lupus erythematosus;

KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;

KW allergic disease; asthma; demyelinating disease;

KW degenerative cartilaginous disorder; transplantation associated disease.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT Peptide 1..23

FT Protein 24..667

FT Region 90..96

FT /label= Mature_IL_17RH3

FT /note= "N-myristoylation site"

FT Region 104..108

FT /note= "cAMP/GMP-dependent protein kinase phosphorylation site"

FT Modified-site 318..322

FT /note= "Asn is N-glycosylated"

FT Region 322..329

FT /note= "Tyrosine kinase phosphorylation site"

FT Modified-site 347..351

FT /note= "Asn is N-glycosylated"

FT Region 358..364

FT /note= "N-myristoylation site"

FT Modified-site 364..368

FT /note= "Asn is N-glycosylated"

FT Region 453..462

FT /note= "Eukaryotic cobalamin-binding protein motif"

FT Domain 455..472

FT /note= "Transmembrane domain"

FT Region 470..476

FT /note= "N-myristoylation site"

FT Region 482..486

FT /note= "Glycosaminoglycan attachment site"

FT Region 645..649

FT /note= "cAMP/GMP-dependent protein kinase phosphorylation site"

XX WO200146420-A2.

XX 28-JUN-2001.

XX 20-DEC-2000; 2000WO-US34956.

XX 23-DEC-1999; 99US-0172096.

XX 30-DEC-1999; 99WO-US31274.

XX 11-JAN-2000; 2000US-0175481.

XX 18-FEB-2000; 2000WO-US04341.

XX 02-MAR-2000; 2000WO-US05841.

XX 21-MAR-2000; 2000US-0191007.

XX 21-MAR-2000; 2000WO-US07532.

XX 02-JUN-2000; 2000WO-US15264.

XX 22-JUN-2000; 2000US-0213087.

XX 22-AUG-2000; 2000US-0644848.

XX 24-AUG-2000; 2000WO-US23328.

XX 24-OCT-2000; 2000US-0242837.

XX 10-NOV-2000; 2000WO-US30873.

XX 28-NOV-2000; 2000US-0253646.

XX 01-DEC-2000; 2000WO-US32678.

XX (GETH) GENENTECH INC.

XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;

PI Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL;

PI Watanabe CK, Williams PW, Wood WI, Yansura DG;

XX

DR WPI; 2001-451708/48.
 XX N-PSDB; AAS09516.
 PT Novel PRO polypeptides homologous to interleukin-17, useful for the
 PT diagnosis and treatment of immune related disease e.g. rheumatoid
 XX arthritis and diabetes -
 PS Claim 10; Fig 16; 188pp; English.
 XX
 CC The sequence is PRO9877 which is the human Interleukin 17 receptor,
 CC IL-17RH3, encoded by DNA 119502-2789. A composition
 CC containing ant/agonists to the PRO polypeptides or individual components
 CC are useful for treating a mammal with an immune related disease, e.g.
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease, an autoimmune or immune-mediated skin
 CC disease, contact dermatitis, an allergic disease e.g. food
 CC hypersensitivity, asthma, a transplantation associated disease, or a
 CC chronic inflammatory demyelinating polynuropathy. Treating a
 CC degenerative cartilaginous disorder comprises administering a PRO1031 or
 CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous
 CC examples of the diseases and disorders are given in the specification.
 XX
 SQ Sequence 667 AA;

Query Match 77.2%; Score 2711; DB 22; Length 667;
 Best Local Similarity 77.5%; Pred. No. 2e-239;
 Matches 548; Conservative 15; Mismatches 54; Indels 90; Gaps 11;

QY 1 MGSSRLAALLPLLLIVIDLSDSAGIGRHLPHNTRCPPLASHTEVLPISLAAPGGPSP 60
 DB 1 MGSSRLAALLPLLLIVIDLSDSAGIGRHLPHNTRCPPLASHTEVLPISLAAPGGPSP 60
 QY 61 QSLGVCESGTPAVNCASCCQVAFNGASSTSCRNPKSLPHSSISGDTRCQHL----- 116
 DB 46 -----DSFTGSSAYIPCRTWAL--FSTKPMK--VRVWHCSS--CLCQHLSSGGS 89
 QY 117 ---RGSCLVVTCRLRAITF-----PSPQTS--PTRDFALKGNLRIQRHGKVPDP 163
 DB 90 GLQGLFLHLLVQKSKSTFFRYRHKKMPAPAQRKLLPRRHLSKSHIISPS-----PD 144
 QY 164 WTHGM-----EVGTGYNNRWQLSGGPEFSDLLPEARAIRVTISSGPEVSRL 213
 DB 145 ISHGLRSKRTPQSDPETWESLPRLDQSORHGGPEFSDLLPEARAIRVTISSGPEVSRL 204
 QY 214 CHQWALECEELSSPYDQKIVSGGHTVELPEFLLPCLCIEASYLQEDTVRRKKCPQSQW 273
 DB 205 CHQWALECEELSSPYDQKIVSGGHTVELPEFLLPCLCIEASYLQEDTVRRKKCPQSQW 264
 QY 274 PEAYGSDFWKSVHFTDYSHQTMVYALTLRCPLKLEALCORHDWHTLCKDLNPATARES 333
 DB 265 PEAYGSDFWKSVHFTDYSHQTMVYALTLRCPLKLEALCORHDWHTLCKDLNPATARES 324
 QY 334 DGWVLEKVDLHPOLCFKVPWFSEFGNSSHVECPHQTSITSNMNSMDTQAQQLILHFS 393
 DB 325 DGWVLEKVDLHPOLCFK----FSGNSSHVECPHQTSITSNMNSMDTQAQQLILHFS 380
 QY 394 RMHATFSAANSLPGLGDTLVPPVYTSQ-----VWRSQVQF 430
 DB 381 RMHATFSAANSLPGLGDTLVPPVYTSQARGSPVSLDLIIPFLPGCCVLVWRSQVQF 440
 QY 431 AKWHLCPDVSRYHGLLILALLALLTLGLVLAALTCRRPQSGPGPARPVLLHAAADSEA 490
 DB 441 AKWHLCPDVSRYHGLLILALLALLTLGLVLAALTCRRPQSGPGPARPVLLHAAADSEA 500
 QY 491 QRLVGAALAEALLRAALGGGRDVIDLWEGRHVARVGLPWLWAARTVAREQGTVLLWS 550
 DB 501 QRLVGAALAEALLRAALGGGRDVIDLWEGRHVARVGLPWLWAARTVAREQGTVLLWS 560
 QY 551 GADLRPVSGDPPRAAPLLALLHAAPRLLLLAYFSRLCAKGDIPPLRALPYRLLRDLP 610

Db 561 GADLRPVSGDPPRAAPLLALLHAAPRLLLLAYFSRLCAKGDIPPLRALPYRLLRDLP 620
 QY 611 RLLRALDARPAEATSWGRLGARORRQSRLELCSRLEREARLADLG 657
 DB 621 RLLRALDARPAEATSWGRLGARORRQSRLELCSRLEREARLADLG 667

RESULT 3
 AAU83601
 ID AAU83601 standard; Protein; 667 AA.
 AC AAU83601;
 XX
 DT 08-MAY-2002 (first entry)
 XX Human PRO protein, Seq ID No 20.
 DE
 XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.
 XX
 OS Homo sapiens.
 XX
 PN WO200208288-A2.
 XX
 PD 31-JAN-2002.
 XX
 XX 29-JUN-2001; 2001WO-US21066.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001WO-US17092.
 XX
 XX (GETH) GENENTECH INC.
 PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI: 2002-172001/22.
 DR N-PSDB; ABK33545.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX
 XX Claim 11; Figure 20; 359pp; English.
 PS
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung

CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AA083592-AA083713 represent human PRO
CC protein sequences of the invention.

XX SQ Sequence 667 AA;

Query Match 77.2%; Score 2711; DB 23; Length 667;
Best Local Similarity 77.5%; Pred. No. 2e-239;
Matches 548; Conservative 15; Mismatches 54; Indels 90; Gaps 11;

QY 1 MGSRLAALLPLLLIVIDLSDSAGIGFRLPHWNTCPPLASHTVLPISLAAPGPGSSP 60

Db 1 MGSRLAALLPLLLIVIDLSDSAGIGFRLPHWNTCPPLASHTD----- 45

QY 61 QSLGVCESGTVPAVCASICQVAFNGASSTWCNRPKSLPHSSSIGDTRCOHLL----- 116

Db 46 -----DSFTGSSAVIPCTWAL--FSTKPCW---VRVHCSSR---CLCQHLLSGGS 89

QY 117 ---RGSCCLVVTCLRRATF-----PSPQTS--PTRDFALKGNPLRIQRHGKVFDP 163

Db 90 GLQGLFHLVQSKSKSTEFYRHKMPAPAKRLPRRLHSEKSHHTIPS-----PD 144

QY 164 WTHKGM-----EVGTGYRRWVQLSGGPEFSDLLPEARAIKVTISSGPEVSRL 213

Db 145 ISHGLSKRTPQSPDETWSLPLDLSQRHGPEFSDLLPEARAIKVTISSGPEVSRL 204

QY 214 CHQWALECEELSSPDYQKIVSGHTVELPEYELLPCICEASYLQEDTVRRKKCFQSW 273

Db 205 CHQWALECEELSSPDYQKIVSGHTVELPEYELLPCICEASYLQEDTVRRKKCFQSW 264

QY 274 PEAYGDFWKSVDYDYSQHTQMYMALTLRCPLKLEALCQRHDWHTLCKDLNPATARES 333

Db 265 PEAYGDFWKSVDYDYSQHTQMYMALTLRCPLKLEALCQRHDWHTLCKDLNPATARES 324

QY 334 DGWVLEKVDLHPOLCFKQVWFSGNSHVCEPHQTSNVSMDTQAQQLILHFSS 393

Db 325 DGWVLEKVDLHPOLCFK-----FSGNSHVCEPHQTSNVSMDTQAQQLILHFSS 380

QY 394 RMHATFSAWSLPGIGQDTLPPVTVTSQ-----VWRSVDQF 430

Db 381 RMHATFSAWSLPGIGQDTLPPVTVTSQARGSSPVSLDLIIPRLPGCCVWVWRSVDQF 440

QY 431 AWKHLCPDVSRYHGLLLILALLTLGLLVVLTALTCRRPQSGPGPARVLLHAADSEA 490

Db 441 AWKHLCPDVSRYHGLLLILALLTLGLLVVLTALTCRRPQSGPGPARVLLHAADSEA 500

QY 491 ORRVINGALAEALLRAALGGGRDVIDLMEGRHVARVGLPWLWARTVAREOGTVLLWS 550

Db 501 ORRVINGALAEALLRAALGGGRDVIDLMEGRHVARVGLPWLWARTVAREOGTVLLWS 560

QY 551 GADLRPVSGPDPRAAPLALLHAAPRPLLLLAYFSRLCAKGDIPPLRALPRYLLRLDLP 610

Db 561 GADLRPVSGPDPRAAPLALLHAAPRPLLLLAYFSRLCAKGDIPPLRALPRYLLRLDLP 620

QY 611 RLLRALDARPAEATSWGRLGARQRQRSLRLEICSRLEAREARLADLG 657

Db 621 RLLRALDARPAEATSWGRLGARQRQRSLRLEICSRLEAREARLADLG 667

RESULT 4

AAAY76048

ID AAAY76048 standard; Protein: 617 AA.

XX AC AAAY76048;

XX AC AAAY76048;

27-MAR-2000 (first entry)

Murine skin cell protein, SEQ ID NO:303.

XX Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
XX embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
XX secreted; transmembrane; inflammation; cancer; neurological disease;
XX angiogenesis; tumour vascularisation; growth disorder;
XX developmental disorder; skin wound; hair follicle disorder;
XX anti-inflammatory; cytostatic; neuroprotective; vulnery.

OS Mus sp.

XX WO9955865-A1.

XX 04-NOV-1999.

XX 29-APR-1999; 99WO-NZ00051.

XX 29-APR-1998; 98US-0069726.

XX 09-NOV-1998; 98US-0188930.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;

XX WPI; 2000-072177/06.

XX N-PSDB; AAZ61753.

XX Novel polynucleotides useful for the treatment of various conditions
XX including wounds and cancer -

XX Claim 4; Page 179-180; 235pp; English.

XX The invention relates to novel nucleic acid sequences derived from rat
XX dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
XX and mouse embryonic skin. Keratinocyte stem cells and transit amplifying
XX cells. Polypeptides of the invention may be used to treat inflammation,
XX cancer and neurological diseases. The proteins may be used to stimulate
XX the growth and motility of keratinocytes, to inhibit the growth of
XX cancer cells, to modulate angiogenesis and tumour vascularisation, to
XX modulate skin inflammation, to modulate epithelial cell growth and to
XX inhibit binding of HIV-1 to leukocytes. The invention may also be used
XX to treat growth and developmental defects, skin wounds and hair follicle
XX disorders. Sequences AAY75942-Y76123 represent polypeptides encoded
XX by cDNA sequences derived from several mouse, rat or human skin cell
XX types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and
XX AAY76119 are proteins with an N-terminal signal sequence, indicating
XX that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,
XX AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
XX putative transmembrane domains.

XX SQ Sequence 617 AA;

Query Match 52.1%; Score 1831.5; DB 21; Length 617;

Best Local Similarity 57.7%; Pred. No. 8.4e-159;

Matches 392; Conservative 49; Mismatches 133; Indels 105; Gaps 10;

QY 1 MGSRLAALLPLLLIVIDLSDSAGIGFRLPHWNTCPPLASHTVLPISLAAPGPGSSP 60

Db 1 MGSRLAALLPLLLIVIDLSDSAGIGFRLPHWNTCPPLASHTVLPISLAAPGPGSSP 60

QY 61 QSLGVCESGTVPAVCASICQVAFNGASSTWCNRPKSLPHSSSIGDTRC-----QHLL 116

Db 46 KRFAGLQWGFPL-----VRKSKPPKFEDYWRHRTPASFORKL 85

QY 117 RGSCCLVVTCLRRATFPSPQTSPTDFALKGNPLRIQRHGKVFDPDTHKMGVEVTGN 176

Db 86 LGSPSLSESHR--ISIP-----AISHRGQTRKRAQPSAAEGREHLPEAGS--- 131

QY 177 RRVQLSGGPEFSDLLPEARAIKVTISSGPEVSRLCHOWALECEELSSPDYQKIVSG 236

Db 132 ----QKGGPEFSDLLPEVQAVRVTPAGPKASVRLCYQWALECEDLSLSPFTQKIVSG 187

CC mammalian skin cells. The polypeptide is useful for stimulating
 CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
 CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
 CC tumours, modulating skin inflammation, stimulating the growth of
 CC epithelial cells, inhibiting the binding of human immunodeficiency virus
 CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
 CC neurological diseases. The polynucleotide can be used as a marker, in
 CC the identification of genetic disorders, and for the design of
 CC oligonucleotides for examining expression patterns.

Query Match 52.1%; Score 1831.5; DB 22; Length 617;
 Best Local Similarity 57.7%; Pred. No. 8.4e-159;
 Matches 392; Conservative 49; Mismatches 133; Indels 105; Gaps 10;

QY 1 MGSSRLAALLPLLLIIVIDLSDSAGIGRHLPHWNTCPCLASHTVEVLPISLAAPGGSPSP 60
 DB 1 MGSPRLAALLPLLLIIVIDLSDSAGIGRHLPHWNTCPCLASHTVEVLPISLAAPGGSPSP 60
 QY 61 QSLGVCESGTPVAVCASICCCQVAFNGASSTSWCRNPKSLPHSSSISGIDTRC---QHLL 116
 DB 46 KRFAGLQWGFLL-----VRKSKPPKFEEDYWRHRTTASQFQKL 85
 QY 117 RGSCCLVVTCLRAITFPSPQSPTRDFALKGNLRIORHGKVFDPWTHKGMEVGTGN 176
 DB 86 LGSFSLSEESHRR--ISIPSS-----AISHRGQRTKRAQPSAAEGREHLPEAGS--- 131
 QY 177 RRVQLSGGPEFSFDLLPEARAIRVTISSGPEVSVRLCHOWALECEELSPYDVQKIVSG 236
 DB 132 ---QKCGPEFSFDLLPEQAVRVITPAGKASVRLCYQWALECEDLSPEPTQKIVSG 187
 QY 237 GHTVELPYEFLPLCLCEIASYLOEDTVRRKKCPQSWPEAYGSDFWKSVHFHTDYSQHTQM 296
 DB 188 GHTVDLPYEFLPLCLCEIASYLOEDTVRRKKCPQSWPEAYGSDFWQSIREFTDYSQHNQM 247
 QY 297 VMALTRCPLKLEAALCORHWHITCKDLPNATARESDGWYLVKVDLHPQLCFKVPWF 356
 DB 248 VMALTRCPLKLEAALCORHWHITCKDLPNATARESDGWYLVKVDLHPQLCFKVPWF 356
 QY 357 SFGNSSHVECPHOTGSLTSWNVSMDTQAQQLILHFSRMRHATFSAWSLPLGLGDTLVP 416
 DB 304 SPENSSHVECPHOTGSLTSWNVSMDTQAQQLILHFSRMRHATFSAWSLPLGLGDTLVP 416
 QY 417 VYTVSQ-----VWRSVQFAWKHLKCPDVSYRHLGLLILALL 453
 DB 364 VYSISQTSQSVPTLDTLIIFFLRQENCILVWRSVDFHFAWKHVLCPDAPYPTQLLRSL- 422
 QY 454 ALLTLGVVLTCTRRPQSGPGPARPVLLLHAADSEAQRRLVGALEALLRAALGGGROVI 513
 DB 423 -----GSGRTFVLLLHAADSEAQRRLVGALEALLRAALGGGROVI 463
 QY 514 VDLWEGHVARVGLPWLWAARTRVAREQGTVLLWSGADLRPVSGPDPRAAPLLALLHA 573
 DB 464 VDLWEGHVARVGLPWLWAARTRVAREQGTVLLWSGADLRPVSGPDPRAAPLLALLHA 573
 QY 574 APRPILLLAYFSLCAKAGDIPPLRALPRYLLRDLPRLLRALDARPAEATSWGRLGAR 633
 DB 524 APRP-LLLAYFSLCAKAGDIPPLRALPRYLLRDLPRLLRALDARPAEATSWGRLGAR 633
 QY 634 QRRQSRLELCSLREAREAR 652
 DB 583 RCLKNRLEQCHLLELEAAK 601

RESULT 6
 AAB55987
 ID AAB55987 standard; Protein; 617 AA.
 AC AAB55987;
 DT 08-MAR-2001 (first entry)
 DE Skin cell protein, SEQ ID NO: 303.
 KW Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV;
 KW neotropic; neuroprotective; vulnerary; immunomodulatory; vaccine;
 KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
 KW inflammation; neurological disease.
 OS Mus sp.
 PN WO200069884-A2.
 XX 23-NOV-2000.
 XX 15-MAY-2000; 2000WO-NZ00075.
 XX 14-MAY-1999; 99US-0312283.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 XX Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;
 XX WPI; 2001-007495/01.
 XX N-PSDB; AAC99686.
 XX New isolated polynucleotide used in the identification of genetic
 XX disorders and encoding polypeptides used for treating inflammatory
 XX disease, cancer and neurological diseases -
 PS Claim 4; Page 244-245; 952pp; English.
 XX The present sequence is a polypeptide which is expressed in

CC mammalian skin cells. The polypeptide is useful for stimulating
 CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
 CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
 CC tumours, modulating skin inflammation, stimulating the growth of
 CC epithelial cells, inhibiting the binding of human immunodeficiency virus
 CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
 CC neurological diseases. The polynucleotide can be used as a marker, in
 CC the identification of genetic disorders, and for the design of
 CC oligonucleotides for examining expression patterns.

Query Match 52.1%; Score 1831.5; DB 22; Length 617;
 Best Local Similarity 57.7%; Pred. No. 8.4e-159;
 Matches 392; Conservative 49; Mismatches 133; Indels 105; Gaps 10;

QY 1 MGSSRLAALLPLLLIIVIDLSDSAGIGRHLPHWNTCPCLASHTVEVLPISLAAPGGSPSP 60
 DB 1 MGSPRLAALLPLLLIIVIDLSDSAGIGRHLPHWNTCPCLASHTVEVLPISLAAPGGSPSP 60
 QY 61 QSLGVCESGTPVAVCASICCCQVAFNGASSTSWCRNPKSLPHSSSISGIDTRC---QHLL 116
 DB 46 KRFAGLQWGFLL-----VRKSKPPKFEEDYWRHRTTASQFQKL 85
 QY 117 RGSCCLVVTCLRAITFPSPQSPTRDFALKGNLRIORHGKVFDPWTHKGMEVGTGN 176
 DB 86 LGSFSLSEESHRR--ISIPSS-----AISHRGQRTKRAQPSAAEGREHLPEAGS--- 131
 QY 177 RRVQLSGGPEFSFDLLPEARAIRVTISSGPEVSVRLCHOWALECEELSPYDVQKIVSG 236
 DB 132 ---QKCGPEFSFDLLPEQAVRVITPAGKASVRLCYQWALECEDLSPEPTQKIVSG 187
 QY 237 GHTVELPYEFLPLCLCEIASYLOEDTVRRKKCPQSWPEAYGSDFWKSVHFHTDYSQHTQM 296
 DB 188 GHTVDLPYEFLPLCLCEIASYLOEDTVRRKKCPQSWPEAYGSDFWQSIREFTDYSQHNQM 247
 QY 297 VMALTRCPLKLEAALCORHWHITCKDLPNATARESDGWYLVKVDLHPQLCFKVPWF 356
 DB 248 VMALTRCPLKLEAALCORHWHITCKDLPNATARESDGWYLVKVDLHPQLCFKVPWF 356
 QY 357 SFGNSSHVECPHOTGSLTSWNVSMDTQAQQLILHFSRMRHATFSAWSLPLGLGDTLVP 416
 DB 304 SPENSSHVECPHOTGSLTSWNVSMDTQAQQLILHFSRMRHATFSAWSLPLGLGDTLVP 416
 QY 417 VYTVSQ-----VWRSVQFAWKHLKCPDVSYRHLGLLILALL 453
 DB 364 VYSISQTSQSVPTLDTLIIFFLRQENCILVWRSVDFHFAWKHVLCPDAPYPTQLLRSL- 422
 QY 454 ALLTLGVVLTCTRRPQSGPGPARPVLLLHAADSEAQRRLVGALEALLRAALGGGROVI 513
 DB 423 -----GSGRTFVLLLHAADSEAQRRLVGALEALLRAALGGGROVI 463
 QY 514 VDLWEGHVARVGLPWLWAARTRVAREQGTVLLWSGADLRPVSGPDPRAAPLLALLHA 573
 DB 464 VDLWEGHVARVGLPWLWAARTRVAREQGTVLLWSGADLRPVSGPDPRAAPLLALLHA 573
 QY 574 APRPILLLAYFSLCAKAGDIPPLRALPRYLLRDLPRLLRALDARPAEATSWGRLGAR 633
 DB 524 APRP-LLLAYFSLCAKAGDIPPLRALPRYLLRDLPRLLRALDARPAEATSWGRLGAR 633
 QY 634 QRRQSRLELCSLREAREAR 652
 DB 583 RCLKNRLEQCHLLELEAAK 601

RESULT 6
 AAB55987
 ID AAB55987 standard; Protein; 617 AA.
 XX AAB55987;
 AC AAB55987;
 XX DT 04-APR-2002 (first entry)
 XX

DE	Murine protein isolated from skin cells SEQ ID NO: 303.	
XX	Human; rat; mouse; skin cell; skin wound; cancer; growth defect;	
KW	developmental defect; inflammatory disease; dermatological; vulnary;	
KW	immunomodulator; anti-inflammatory; cytostatic; neuroprotective.	
OS	Mus sp.	
XX	WO200190357-A1.	
PN	29-NOV-2001.	
PD	24-MAY-2001; 2001WO-NZ00099.	
XX	24-MAY-2000; 2000US-206650P.	
XX	25-JUL-2000; 2000US-221232P.	
PR	(GENE-) GENESIS RES & DEV CORP LTD.	
XX	Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;	
PI	WPI; 2002-122020/16.	
DR	New polynucleotides and polypeptides encoded by the polynucleotides	
XX	isolated from skin cells, useful for treating skin wounds, cancers,	
PT	growth and developmental defects, inflammatory diseases, or for	
PT	modulating immune responses	
PT	Example 2; Page 200-201; 466pp; English.	
XX	The present invention provides the protein and coding sequences of cDNAs	
PS	isolated from human, murine and rat skin cell libraries. The sequences	
XX	can be used in the development of therapeutic agents useful in the	
CC	treatment of skin diseases, including skin wounds, cancer, growth	
CC	defects, developmental defects and inflammatory diseases. The proteins	
CC	have important roles in the induction of hair growth, cell proliferation	
CC	and cell-cell interaction, in maintaining tissue integrity, in wound	
CC	healing and in modulating immune responses. The present sequence is a	
CC	polypeptide of the invention.	
XX	Sequence 617 AA;	
SQ	Query Match 52.1%; Score 1831.5; DB 23; Length 617;	
	Best Local Similarity 57.7%; Pred. No. 8.4e-159;	
	Matches 392; Conservative 49; Mismatches 133; Indels 105; Gaps 10;	
QY	1 MGSRRLAALLPPLLIVLSDSAGIGFPHLPHWNTCRPLASHTEVLPISLAAPGSPSP 60	
Db	1 MGSPRLAALLLSLPLLLIGLAVSARVACPLRSWTSKCLLAYRVD----- 45	
QY	61 QSLGVCESTVPVAVCASICQVAVNGASSTSWCRNPKSLPHSSSIGDTRC---QHLL 116	
Db	46 KRFAQLQWGFPL-----VKSKSPKFDYWRHRTFASFQRL 85	
QY	117 RGSCLVVTCLRRATFPSPSPOTSPTDFALKGNLRIQRHGKVPDPDTHKMEVGTGYN 176	
Db	86 LGSPLSESHR--ISIPSS-----AISHRGQRTKRAQPSAAEGREHLPEAGS--- 131	
QY	177 RRVVQLSGGPEFEDLLPEARATRVISSGPEVSVRLCHOWALECELSPPYDVQKIVSS 236	
Db	132 ----QKGGPEFDFLLPEQAVRVTPAGPKASVRLCQWALECELSPPFTQKIVSG 187	
QY	237 GHTVELPYEFLPCLEASYLOEDTVRRKKCFQSWPEAYGSDFKWSVHFTDYSQHTQM 296	
Db	188 GHTVDLPYELLPCMCLEASYLOEDTVRRKKCFQSWPEAYGSDFWQSIREFDYSQHNQM 247	
QY	297 VMALTLRCLPLKLEAACQORHWHITCKDLPNATARSQGVYVLEKVDLHPQLCFKVPWF 356	
Db	248 VMALTLRCLPLKLEASLCWRQDPLTPCETLPNATAQSEGWYILENVDLHPQLCFK----F 303	
QY	357 SFGNSSHVECPHQGTSNNVSMDTAQQLILHFSRHMATFSAAWSLPLGQDTLVPP 416	
Db	304 SFENSSHVECPHOGSLPSTWTSMDTQAOQLTLHFSKRYATFSAAWSDFGLGPTFMPP 363	

QY	417 VYTVSQ-----VWRSDVQFAWKHLCPDVSYRHLGLLALL 453	
Db	364 VYSISQTQSGVPVTLDLIIPFLRQENCILVWRSDVHFAMKVLCPDDAPYPTQLLRSL- 422	
QY	454 ALLTLGVVALTCRRPQSGPGPARPVLLLHHAADSAQRRLVGALAEELRAALGGGRDVI 513	
Db	423 -----GSGTRPVLHHAADSAQRRLVGALAEELRTALGGGRDVI 463	
QY	514 VDLWEGHVARVGPLWLWAARTVRAREQGTVLLWSGADLRPVSGPDPRAPFLALLHA 573	
Db	464 VDLWEGTHVARIIGLPLWLWAARVAREQGTVLLWNCACGPSTACSGDQQAASLRTLLCA 523	
QY	574 APRPLLLAYFSLCAKGDIPPLRALPRYRLRLDLPRLRALDARPFABATSWGRLGAR 633	
Db	524 APRP-LLLAYFSLCAKGDIPPLRALPRYRLRLDLPRLRALDAQPATVLIASSWSHLGAK 582	
QY	634 QRRQSRLELCSRLEREAAAR 652	
Db	583 RCLKNRLEQCHLLEAAK 601	
RESULT 7		
AAU83238	AAU83238 standard; Protein; 226 AA.	
XX	AAU83238;	
AC	08-MAY-2002 (first entry)	
XX	Novel secreted protein Z935805G4P.	
DT	Protein secretion; mammalian secreted polypeptide; MSP.	
DE	Homo sapiens.	
XX	WO200202621-A2.	
XX	10-JAN-2002.	
XX	28-JUN-2001; 2001WO-US20638.	
XX	30-JUN-2000; 2000US-215446P.	
XX	(ZYMO) ZYMOGENETICS INC.	
PA	Sheppard PO, Presnell SR;	
PI	WPI; 2002-147999/19.	
XX	N-PSDB; ABK33153.	
DR	Novel isolated mammalian secreted polypeptide useful in therapeutic and	
XX	diagnostic methods, to direct secretion of other proteins of interest	
PT	from host cell, as educational tools, and as laboratory practicum kits	
PT	Claim 12; Page 396-397; 397pp; English.	
XX	The invention describes an isolated mammalian secreted polypeptide (MSP)	
CC	(I). (I) is useful to direct the secretion of other proteins of interest	
CC	from a host cell, to monitor secretion of proteins, to degenerate	
CC	sequences comprising all nucleotide sequences encoding a particular	
CC	polypeptide, to screen for cell metabolism effecting receptors, for	
CC	identifying new target receptors and drug design, for identifying, for	
CC	protein purification, for determining the weight of expressed MSP	
CC	polypeptides as a ratio to total protein expressed, for identifying	
CC	peptide cleavage sites, for coupling amino and carboxy terminal tags, for	
CC	amino acid sequence analysis, for monitoring biological activities of the	
CC	protein in vitro and in vivo, and to teach analytical skills and as	
CC	reagents for the study of cells, receptors, and other binding molecules.	
CC	The polynucleotide is useful for radiation hybrid mapping, and somatic	
CC	cell genetic technique developed for constructing high-resolution,	
CC	contiguous maps of mammalian chromosomes. Reagents disclosed in the	

PA (GENE-) GENESIS RES & DEV CORP LTD.
XX Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;
PI WPI; 2001-007495/01.
XX
DR
XX
XX New isolated polynucleotide used in the identification of genetic
PT disorders and encoding polypeptides used for treating inflammatory
PT disease, cancer and neurological diseases -
XX
XX
PS Claim 4; Page 136-137; 352pp; English.
XX
XX The present sequence is a polypeptide which is expressed in
CC mammalian skin cells. The polypeptide is useful for stimulating
CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC tumours, modulating skin inflammation, stimulating the growth of
CC epithelial cells, inhibiting the binding of human immunodeficiency virus
CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
CC neurological diseases. The polynucleotide can be used as a marker, in
CC the identification of genetic disorders, and for the design of
CC oligonucleotides for examining expression patterns.
XX
SQ Sequence 330 AA;
Query Match 27.0%; Score 948.5; DB 22; Length 330;
Best Local Similarity 53.2%; Pred. No. 3.2e-78;
Matches 206; Conservative 31; Mismatches 89; Indels 61; Gaps 7;
QY 1 MGSSRLAALLPLLLIIVLSDSAGIGRHLPHWNTCRPLASHTEVLPISLAAPGGPSSP 60
DB 1 MGSPRLAALLSLPLLLIGLAVSARVACPCLSRWSHCLLAYRVD----- 45
QY 61 QSLGVCESGTVPAVCASICQVAVNGASSTWCNRPKSLPHSSSIGDTRC----QHLL 116
DB 46 KRFAGLQWGFPLL-----VRKSKPPKFEDYWRHRTPASFORKL 85
QY 117 RGSCLLVVTCRLRAITFPSPPTSPTRDFALKGNLRIQRHGKVFDPWTHKGMEVGTGN 176
DB 86 LGSPSLSESHR--ISIPSS-----AISHRGQRTKRAQPSAAEGREHLPEAGS--- 131
QY 177 RRWVQLSGGPEFSDLLPEARIRVTISSGPEVSVRLCHQWALECEELSSPDYQKIVSG 236
DB 132 ----QKCGGPEFSDLLPEVQAVRTIPAGPKASVRLCYQWALECEDLSSPDTQKIVSG 187
QY 237 GHTVLPYEFLLPCLCIEASYLQEDTVRRKKCPQSWPEAYGSDFWKSVHFTDYSOHTQM 296
DB 188 GHTVDLPYEFLLPCMCIEASYLQEDTVRRKKCPQSWPEAYGSDFWQSVIRFTDYSOHNQM 247
QY 297 VMALTLRCPKLEAALCQRHDMHTLCKDLPNATARESOGWYVLEKVDLHPQLCFKVPWF 356
DB 248 VMALTLRCPKLEASLCWRQDPLTPCETLPNATAQESGWIILENVDLHPQLCFK----F 303
QY 357 SFGNSSHVECPHOTGSLTSWNVSMDTQ 383
DB 304 SFENSSHVECPHQSGSLPSWTVMMDTQ 330
RESULT 10
ABB72086
ID ABB72086 standard; Protein; 330 AA.
XX
AC ABB72086;
XX
XX
DT 04-APR-2002 (first entry)
XX Murine protein isolated from skin cells SEQ ID NO: 125.
XX Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW developmental defect; inflammatory disease; dermatological; vulvar;
KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective.
XX
OS Mus sp.

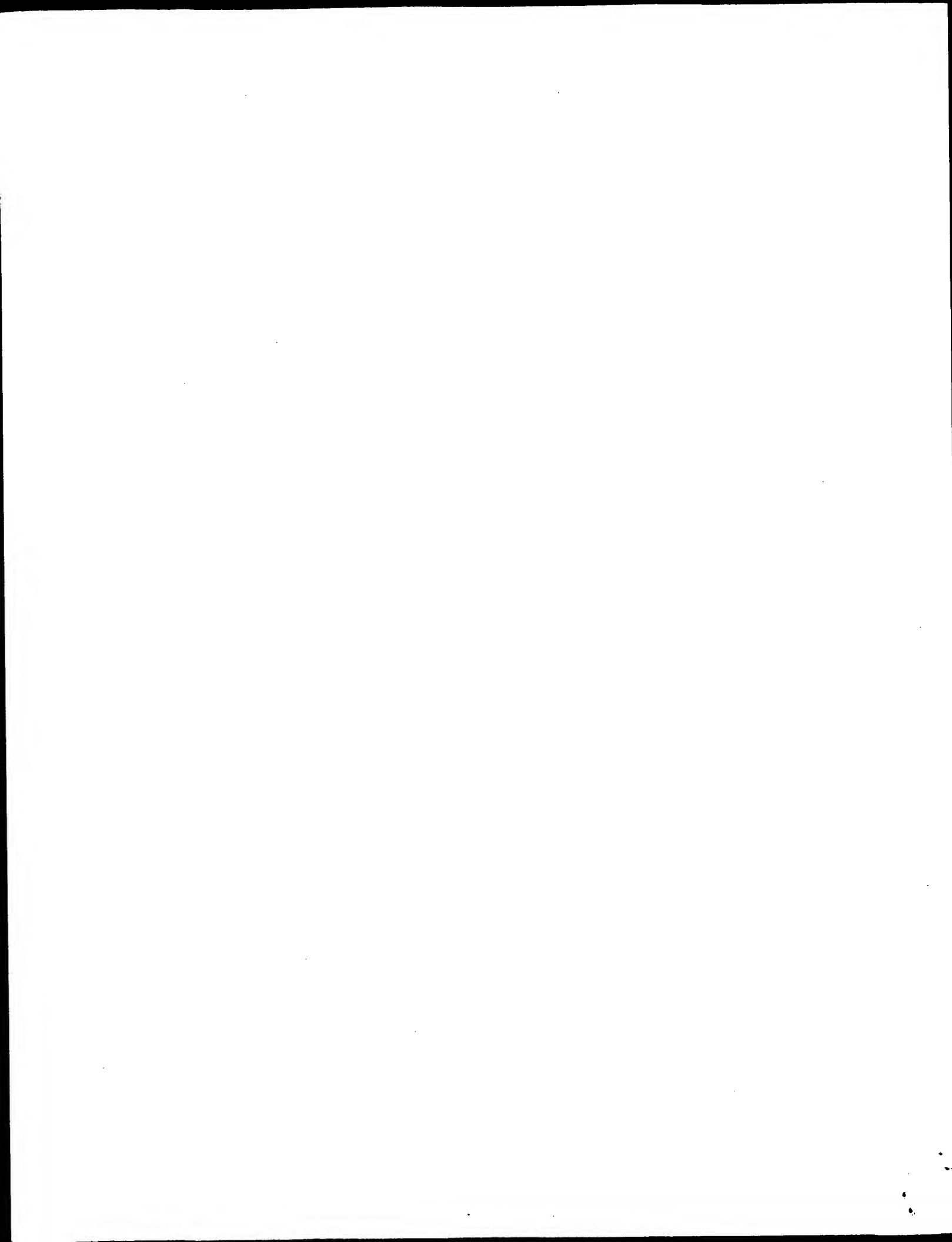
XX
PN WO200190357-A1.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-NZ00099.
XX
PR 24-MAY-2000; 2000US-206650P.
XX
PR 25-JUL-2000; 2000US-221232P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;
PI WPI; 2002-122020/16.
XX
XX New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,
PT growth and developmental defects, inflammatory diseases, or for
PT modulating immune responses -
XX
XX Example 2; Page 118-119; 466pp; English.
XX
XX The present invention provides the protein and coding sequences of cDNAs
CC isolated from human, murine and rat skin cell libraries. The sequences
CC can be used in the development of therapeutic agents useful in the
CC treatment of skin diseases, including skin wounds, cancer, growth
CC defects, developmental defects and inflammatory diseases. The proteins
CC have important roles in the induction of hair growth, cell proliferation
CC and cell-cell interaction, in maintaining tissue integrity, in wound
CC healing and in modulating immune responses. The present sequence is a
CC polypeptide of the invention.
XX
SQ Sequence 330 AA;
Query Match 27.0%; Score 948.5; DB 23; Length 330;
Best Local Similarity 53.2%; Pred. No. 3.2e-78;
Matches 206; Conservative 31; Mismatches 89; Indels 61; Gaps 7;
QY 1 MGSSRLAALLPLLLIIVLSDSAGIGRHLPHWNTCRPLASHTEVLPISLAAPGGPSSP 60
DB 1 MGSPRLAALLSLPLLLIGLAVSARVACPCLSRWSHCLLAYRVD----- 45
QY 61 QSLGVCESGTVPAVCASICQVAVNGASSTWCNRPKSLPHSSSIGDTRC----QHLL 116
DB 46 KRFAGLQWGFPLL-----VRKSKPPKFEDYWRHRTPASFORKL 85
QY 117 RGSCLLVVTCRLRAITFPSPPTSPTRDFALKGNLRIQRHGKVFDPWTHKGMEVGTGN 176
DB 86 LGSPSLSESHR--ISIPSS-----AISHRGQRTKRAQPSAAEGREHLPEAGS--- 131
QY 177 RRWVQLSGGPEFSDLLPEARIRVTISSGPEVSVRLCHQWALECEELSSPDYQKIVSG 236
DB 132 ----QKCGGPEFSDLLPEVQAVRTIPAGPKASVRLCYQWALECEDLSSPDTQKIVSG 187
QY 237 GHTVLPYEFLLPCLCIEASYLQEDTVRRKKCPQSWPEAYGSDFWKSVHFTDYSOHTQM 296
DB 188 GHTVDLPYEFLLPCMCIEASYLQEDTVRRKKCPQSWPEAYGSDFWQSVIRFTDYSOHNQM 247
QY 297 VMALTLRCPKLEAALCQRHDMHTLCKDLPNATARESOGWYVLEKVDLHPQLCFKVPWF 356
DB 248 VMALTLRCPKLEASLCWRQDPLTPCETLPNATAQESGWIILENVDLHPQLCFK----F 303
QY 357 SFGNSSHVECPHOTGSLTSWNVSMDTQ 383
DB 304 SFENSSHVECPHQSGSLPSWTVMMDTQ 330
RESULT 11
ABB08185
ID ABB08185 standard; Protein; 353 AA.
XX
AC ABB08185;

XX 13-FEB-2002 (first entry)
 XX Novel human diagnostic protein #8176.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS72372.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID NO 38544; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 353 AA;
 XX
 Query Match 15.6%; Score 547; DB 22; Length 353;
 Best Local Similarity 99.1%; Pred. No. 2.4e-41;
 Matches 107; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 550 SGADLRPVSGDPDRAPIALHAPRPLLLAYFSRLCAKGDIPPLRALPRYLLRLD 609
 DB 246 SGADLRPVSGDPDRAPIALHAPRPLLLAYFSRLCAKGDIPPLRALPRYLLRLD 305
 QY 610 PRLRLDARPAEATSWGRIGARORRORSLCRLREARLADLG 657
 DB 306 PRLRLDARPAEATSWGRIGARORRORSLCRLREARLADLG 353
 RESULT 12
 ABG08183
 ID ABG08183 standard; Protein; 145 AA.

XX ABC08183;
 AC 13-FEB-2002 (first entry)
 XX Novel human diagnostic protein #8174.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS72370.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID NO 38542; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 145 AA;
 XX
 Query Match 12.5%; Score 438; DB 22; Length 145;
 Best Local Similarity 100.0%; Pred. No. 6.4e-32;
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSSRLAALLPLLLIVIDLSDSAGIGFRHLPHNTRCPLASHTEVLPISLAAPGGSSP 60
 DB 1 MGSSRLAALLPLLLIVIDLSDSAGIGFRHLPHNTRCPLASHTEVLPISLAAPGGSSP 60
 QY 61 OSLGVCSGGTVPACVCAICCCQVAQ 84
 DB 61 OSLGVCSGGTVPACVCAICCCQVAQ 84
 RESULT 13

AAU11357
 ID AAU11357 standard; Protein; 243 AA.
 XX AAU11357;
 AC
 XX DT 26-MAR-2002 (first entry)
 XX DE Mouse DNAX cytokine receptor subunit 9 (DCRS9) polypeptide.
 XX KW Mouse; DNAX cytokine receptor subunit 9; DCRS9; phosphate labelling;
 KW gene therapy; protein therapy; immunological disorder.
 XX OS Mus musculus.
 XX PN WO200190358-A2.
 XX PD 29-NOV-2001.
 XX XX 23-MAY-2001; 2001WO-US16767.
 XX PF 24-MAY-2000; 2000US-206862P.
 XX PR (SCHE) SCHERING CORP.
 XX PA Gorman DM;
 XX PI
 XX DR WPI: 2002-106198/14.
 XX DR N-PSDB; AAS18138.
 XX XX Isolated antigenic human or mouse DNAX receptor subunit-like
 PT polypeptide useful for detecting antibodies generated in response to
 PT presence of increased protein levels or immunological disorders -
 XX
 XX Claim 1; Page 32; 148pp; English.
 XX The invention relates to primate and rodent DNAX cytokine receptor
 CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
 CC receptors, or their portions may be useful as phosphate labelling enzymes
 CC to label general or specific substrates. The subunits may also be
 CC functional immunogens to elicit recognising antibodies, or antigens
 CC capable of binding antibodies. A combination, e.g., including a DCRS can
 CC be used as an immunogen for the production of antisera or antibodies
 CC capable of distinguishing between other cytokine receptor family members.
 CC A purified DCRS can also be used as a reagent to detect antibodies
 CC generated in response to the presence of elevated levels of expression,
 CC or immunological disorders which lead to antibody production to the
 CC endogenous receptor. This sequence represents the mouse DCRS9
 CC polypeptide.
 XX
 XX SQ Sequence 243 AA;
 Query Match 12.4%; Score 435.5; DB 23; Length 243;
 Best Local Similarity 41.4%; Pred. No. 2.3e-31;
 Matches 113; Conservative 23; Mismatches 80; Indels 57; Gaps 6;
 QY 1 MGSRLAALLLLPILLIVLSDSAGTGFRHLPHWNTCPPLASHTVLPISLAAPGPPSP 60
 DB 1 MGSPLAALLLLPILLIGLAVSARVACPCLRSWTSHCLLAYRVD----- 45
 QY 61 QSLGVCESGTVPAVCASICQVAQVNGASSTWCNRPKSLPHSSSIGDTRC----OHL 116
 DB 46 KRFAGLQMGWFFLL-----VRKSKSPPKFEDYWRHTPASFQRL 85
 QY 117 RGSCLVVTCLRRRAITPPSPQTSPTDRFALKGNFLRIORHGKVFVDWTHKMGVEGTGYN 176
 DB 86 LGSPSLSESHR--ISIPSS-----AISHRGQRTKRAQPSAAGEHLPKPEAGS--- 131
 QY 177 RRWVQLSGGPEFSDLLPEARATRVISSGPEVSVRLCHOWALECEELSSPYDVQKIVSG 236
 DB 132 ---QKCGGPEFSDLLPEVQAVRVITPAGFKARVRLCYOWALECEELSSPYDVQKIVSG 187
 QY 237 GHTVLEPYEFLPCMCIEASYLQEDTVRRKSP 269
 DB 188 GHTVLEPYEFLPCMCIEASYLQEDTVRRKSP 220

RESULT 14
 ABB72297
 ID ABB72297 standard; Protein; 698 AA.
 XX ABB72297;
 AC
 XX DT 04-APR-2002 (first entry)
 XX DE Murine protein isolated from skin cells SEQ ID NO: 509.
 XX KW Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
 KW developmental defect; inflammatory disease; dermatological; vulnary;
 KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective.
 XX OS Mus sp.
 XX PN WO200190357-A1.
 XX PD 29-NOV-2001.
 XX XX 24-MAY-2001; 2001WO-NZ00099.
 XX PF 24-MAY-2000; 2000US-206650P.
 XX PR 25-JUL-2000; 2000US-22132P.
 XX XX (GENE-) GENESIS RES & DEV CORP LTD.
 XX PA Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;
 XX WPI: 2002-122020/16.
 XX XX New polynucleotides and polypeptides encoded by the polynucleotides
 PT isolated from skin cells, useful for treating skin wounds, cancers,
 PT growth and developmental defects, inflammatory diseases, or for
 PT modulating immune responses -
 XX
 XX Claim 4; Page 314-315; 466pp; English.
 XX The present invention provides the protein and coding sequences of cDNAs
 CC isolated from human, murine and rat skin cell libraries. The sequences
 CC can be used in the development of therapeutic agents useful in the
 CC treatment of skin diseases, including skin wounds, cancer, growth
 CC defects, developmental defects and inflammatory diseases. The proteins
 CC have important roles in the induction of hair growth, cell proliferation
 CC and cell-cell interaction, in maintaining tissue integrity, in wound
 CC healing and in modulating immune responses. The present sequence is a
 CC polypeptide of the invention.
 XX
 XX SQ Sequence 698 AA;
 Query Match 9.1%; Score 318; DB 23; Length 698;
 Best Local Similarity 24.9%; Pred. No. 6.6e-20;
 Matches 177; Conservative 78; Mismatches 299; Indels 156; Gaps 31;
 QY 32 PHWNTCPPLASHTV-----LPISL-AAPGSSPOSILGV-----CESTVPAVCASI 78
 DB 27 PQTARCSLGLSCHLDGDLVCLPGSLOSAPGVLVPTRLQTELVLRCPQKTDCAICVRV 86
 QY 79 CCQVAQVNGASSTWCNRPKSLPHSSSIGDTRCQHLRSGCCLVVTCLRRRAITPPS--- 135
 DB 87 VVHLAVGHWAPEAGKSDSELSERN-ASLQAVVLSFQAYPIARCALLEVQVPADLV 145
 QY 136 -PQTSPTDRF-----ALKGNLRIORHGK-----VFPDTHKMGVEGTGYNRRW 179
 DB 146 QGQSVGSAVDFCEASLGAEEVQIWSYTKPRYQKELNLTQQLPDC--RGLEVRDSIQSCW 203
 QY 180 V-----QLSGGPEFSDL-----LPEARATRVITSSGPEVSVRLCHOWA 218
 DB 204 VLPWLVNVTGDNVLLTLDVSEEDQFSFLLYLRVPVDA-----LKSLLW- 246



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OM protein - protein search, using sw model

Run On: January 28, 2003, 09:28:53 ; Search time 17 Seconds
(without alignments)
1137.109 Million cell updates/sec

Title: US-09-863-818A-12
Perfect score: 3512
Sequence: 1 MGSRLLAALLPLLLIIVDL.....SRLECSRLREARLADLG 657

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1831.5	52.1	617	4	US-09-188-930-303
2	948.5	27.0	310	4	US-09-188-930-125
3	123	3.5	866	2	US-08-620-694A-10
4	123	3.5	866	3	US-09-022-255-10
5	123	3.5	866	3	US-09-022-696-10
6	123	3.5	866	3	US-08-978-773-4
7	123	3.5	866	3	US-09-022-253-10
8	123	3.5	866	3	US-09-022-260-10
9	123	3.5	866	4	US-09-022-259-10
10	123	3.5	866	4	US-09-022-257-10
11	121.5	3.5	864	2	US-08-620-694A-2
12	121.5	3.5	864	3	US-09-022-255-2
13	121.5	3.5	864	3	US-09-022-696-2
14	121.5	3.5	864	3	US-08-978-773-2
15	121.5	3.5	864	3	US-09-022-253-2
16	121.5	3.5	864	3	US-09-022-260-2
17	121.5	3.5	864	4	US-09-022-259-2
18	121.5	3.5	864	4	US-09-022-257-2
19	114.5	3.3	635	1	US-08-184-327A-4
20	114.5	3.3	635	2	US-08-078-311-1
21	114.5	3.3	635	2	US-08-460-402-1
22	114.5	3.3	635	5	PCT-US95-00670-4
23	113.5	3.2	2864	4	US-08-469-260A-394
24	109	3.1	451	1	US-08-570-157-2
25	109	3.1	451	1	US-09-076-510-2
26	107.5	3.1	452	1	US-07-937-609-16
27	107.5	3.1	452	4	US-08-029-170-16

28	104	3.0	1248	4	US-08-882-046-6	Sequence 6, Appl
29	102	2.9	576	4	US-09-367-206-1	Sequence 1, Appl
30	102	2.9	576	4	US-09-367-206-21	Sequence 21, Appl
31	102	2.9	576	4	US-09-367-206-22	Sequence 22, Appl
32	101	2.9	576	4	US-09-367-206-23	Sequence 23, Appl
33	99.5	2.8	3079	4	US-09-413-814-80	Sequence 80, Appl
34	99	2.8	7257	3	US-09-335-409-5	Sequence 5, Appl
35	99	2.8	7257	4	US-09-568-102-5	Sequence 5, Appl
36	99	2.8	7257	4	US-09-567-969-5	Sequence 5, Appl
37	99	2.8	7257	4	US-09-568-486-5	Sequence 5, Appl
38	99	2.8	7257	4	US-09-568-486-5	Sequence 5, Appl
39	99	2.8	7257	4	US-09-568-472-5	Sequence 5, Appl
40	99	2.8	7257	4	US-09-567-899-5	Sequence 5, Appl
41	97	2.8	3072	4	US-09-413-814-93	Patent No. 5223425
42	96.5	2.7	222	6	5223425-6	Sequence 10, Appl
43	96.5	2.7	3724	2	US-08-804-227C-10	Sequence 4, Appl
44	96.5	2.7	3724	2	US-08-804-198-4	Sequence 2, Appl
45	95.5	2.7	2205	1	US-08-093-453B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-188-930-303
; Sequence 303, Application US/09188930A

; Patent No. 6150502

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Christ, Rene

; APPLICANT: Murison, James Greg

; TITLE OF INVENTION: Compositions Isolated From Skin Cells

; FILE REFERENCE: 11000.1011c1

; CURRENT APPLICATION NUMBER: US/09/188,930A

; CURRENT FILING DATE: 1998-11-09

; NUMBER OF SEQ ID NOS: 348

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 303

; LENGTH: 617

; TYPE: PRT

; ORGANISM: Mouse

US-09-188-930-303

Query Match 52.1%; Score 1831.5; DB 4; Length 617;
Best Local Similarity 57.7%; Pred. No. 3.6e-176;
Matches 392; Conservative 49; Mismatches 133; Indels 105; Gaps 10;

QY	1	MGSRLLAALLPLLLIIVDLSDSAGIGFRLPHWNTRCPLASHTEVLPISLAAGGSPSP	60
DB	1	MGSPRLAALLPLLLIIGLAVSARVACPLRSWTSHCLLAYRVD	45
QY	61	QSLGVCSTVPAVCASICQVAQVFNAGASSVSWCRNPKSLPHSSSIGDTRC	116
DB	46	KRFAGLWGFLL	85
QY	117	RGSCCLWTCRLRAITFPSPQTSPTDRFALKGNLRTQHGKVFDPDTHKMGMEVGTGN	176
DB	86	LGSPSLSESHR--TIFPS	131
QY	177	RRWVLSGGPESFOLLPEARIRVITSSGPVSVRLCHQNALECEELSSPYDVQKIVSG	236
DB	132	----QKCGPEFSFOLLPEQAVRTIPAGKASVRLCYQWALECEDLSPPFDTKIVSG	187
QY	237	GHTVELPYEFLPLCLICIASYLQEDTVRRKKCPFOSWPEYSGDFWKSVMHTDYSQHTQM	296
DB	188	GHTVDLPYEFLLPCMCICIASYLQEDTVRRKKCPFOSWPEYSGDFWKSVMHTDYSQHTQM	247
QY	297	VNALTLCRLKLEALCALCRQHDWHTLCKDLPNATARESDGWTYVLEKVDLHPOLCFKVPWF	356
DB	248	VNALTLCRLKLEALCALCRQHDWHTLCKDLPNATARESDGWTYVLEKVDLHPOLCFKVPWF	303

```
QY 357 SFNSHVECPHOTGSLTWNVSDMTQAOQLLHFFSSRMHATESAANSLPGLGDTLVP 416
Db 304 SFNSHVECPHOTGSLTWNVSDMTQAOQLLHFFSSRMHATESAANSLPGLGDTLVP 363
QY 417 VYVSO-----VWRSVQFAWKHLPCPDVSYRHLGLLILALL 453
Db 364 VYISQVTPVTLDDLIIPFLQENCLVWRSVDFHFKHVLCPDDAPYPTQLLRSL- 422
QY 454 ALLTLGVVYALTCRRPQSGPGPARVILLHAADSEARQLVGAELRLAALGGGRDVI 513
Db 423 -----GSGRTPVILLHAADSEARQLVGAELRLAALGGGRDVI 463
QY 514 VDLWGRHVARVCPPLWAAARTVAREQTVLLWAGDLRPVSGPDPRAAPLILALLHA 573
Db 464 VDLWEGTHVARVCPPLWAAARTVAREQTVLLWAGDLRPVSGPDPRAAPLILALLHA 523
QY 574 APRILLAYFSLCAKGDIPPLRALPRYLRLDRLPRLLRALDARPAEATSWRGLGAR 633
Db 524 APR-LLAYFSLCAKGDIPPLRALPRYLRLDRLPRLLRALDARPAEATSWRGLGAR 582
QY 634 QRRQSRLELCRLEREAR 652
Db 583 RCLKNRLEQCHLELEAAK 601

RESULT 2
US-09-188-930-125
; Sequence 125, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 125
; LENGTH: 330
; TYPE: PRT
; ORGANISM: mouse
US-09-188-930-125

Query Match 27.0%; Score 948.5; DB 4; Length 330;
Best Local Similarity 53.2%; Pred. No. 2.3e-87;
Matches 206; Conservative 31; Mismatches 89; Indels 61; Gaps 7;

QY 1 MGSRLAALLPILLIVLSDSAGICFRHLPHWNTRCPPLASHTVLPISLAAPGPPSP 60
Db 1 MGSRLAALLPILLIVLSDSAGICFRHLPHWNTRCPPLASHTVLPISLAAPGPPSP 45
QY 61 QSLGVCESTVPVAVCASICQVAVENGASSTWCNRPKPSLPHSSSIGDTRC-----QHLL 116
Db 46 KRFAGLOWGFPL-----VVKSKSPKPFEDYWRHRTFPASFQRL 85
QY 117 RGSCLLVVTCRRRAITFPSPPTSPTRDFALKGNPLRIQRH-----GKVPF-----DWT 165
Db 86 LGSPLSESHR--ISIPSS-----AISHRGQRTKRAQPSAAEGREHLPEAGS--- 131
QY 177 RRVQLSGGPEFEDLLPEARAIRVTSISPEVSVRLCHOWALECEELSSPYDVQKIVSG 236
Db 132 -----OKCGGPEFEDLLPEARAIRVTSISPEVSVRLCHOWALECEELSSPYDVQKIVSG 187
QY 237 GHTVELPEYFLLPCLEASYLQEDIVRRKKCPFSQWPEAYGSDFWKSVHFDTYSQHTQM 296
Db 188 GHTVDLPYFLLPCMCIEASYLQEDIVRRKKCPFSQWPEAYGSDFWKSVHFDTYSQHTQM 247

QY 297 VMALTRCPLKLEAALCQRHWHTLCKLPNATARESDGWYLVLEKVDLHPQLCFKVPWF 356
Db 248 VMALTRCPLKLEASLCWRQDPLTPCETLPNATAQSEGWYILENDLHPQLCFK----F 303
QY 357 SFNSHVECPHOTGSLTWNVSDMTQ 383
Db 304 SFNSHVECPHOTGSLTWNVSDMTQ 330

RESULT 3
US-09-620-694A-10
; Sequence 10, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-620-694A-10

Query Match 3.5%; Score 123; DB 2; Length 866;
Best Local Similarity 18.0%; Pred. No. 0.0029;
Matches 108; Conservative 74; Mismatches 183; Indels 236; Gaps 26;

QY 116 LRGSCLLVTCRRRAITFPSPPTSPTRDFALKGNPLRIQRH-----GKVPF-----DWT 165
Db 52 VKNSTCLDSDWIHPNLTTPSPK-----DQIQIHLHAHTQOGDLFPVAHIEWT 99
QY 166 -----HKGMEVGT-----CYNRRVQLSGGPSEFSDLLEA 196
Db 100 LOTDASILEGAELSVLQNLNTERLCVRFEEFSLKLRHHRRW-----RFTS----- 147
QY 197 RAIRVTISGPEVSVRLCHOWALECEELSSPYDVQKIVSGGHTVELPEYFLLP----- 249
Db 148 -----HFVDPDQVEYTVHH-----LPKPIPDGDPNNHOSKNFLVPDCEHARM 190
```

QY 250 ---CLCIEASYLOEDTV-----RRKKCPQSWPEAYGSDFWKSVHFTDYSHQHTQWMA 299
Db 191 KVTTPCMSSGSLWDPNITVETLEAHQLRVSTLWNE-----STHYQILLT 235
QY 300 LTLRCPLKLEAALCQRHDWHTLCKDLPNATARESDGWYVLEKVDLHPQLCFKVPWFES-- 357
Db 236 ---SFP-HMENHSCFEH-MHHIPAPRPEEFHQRSNVTLTLRLNKGCCRHQVQIQFFSSC 290
QY 358 ----FGNSHVECPHOTGSLTSWNVSMDTQAQQLILHFSSRMHATFSAWSLPLGQDTL 413
Db 291 LNDCLRHSAIVSCPEM-----PDT 310
QY 414 VPPVTVSVQWRSQVQFAMKHLCPDVSYRHLGLLILALLLTLGLGVVLAITCRPSQG 473
Db 311 EP-----IPDYNPLWVYFETIGSILLVGSVIL-----LIVCMWNR--LAG 349
QY 474 PG-----PA-----RPVLLHAADESAQRRLVGAELALLRAALGGG 509
Db 350 PGSEKYSDDTKYTDGLPAADLIPPLPKPKVWIIYSADHPLYVDVVLKFAQFLLTAC--G 407
QY 510 RDVVDLWEGRHVARVGPPLWMAARTVAREQGTVLLWS-----GADLR- 555
Db 408 TEVALDLLEEQAISEAGVMTWVGROKQEVESNSKIIIVLCSRGTRAKWQALLGRGAPVRL 467
QY 556 -----PVSGPDPRAAPLIALHAAAPR-----LLLAYFSRLCAKGDIPPLRALPYRL 605
Db 468 RCDHGKPVG--DLFTAAMNMILPDFKRPACFGTYVVCYFSEVSCDGDVDFLFGAAPRYPL 525
QY 606 L 606
Db 526 M 526

RESULT 4

US-09-022-255-10
; Sequence 10, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-255-10
Query Match 3.5%; Score 123; DB 3; Length 866;
Best Local Similarity 18.0%; Pred. No. 0.0029;
Matches 108; Conservative 74; Mismatches 183; Indels 236; Gaps 26;
QY 116 LRSGCCLVVTCLRRATITFPSPPTSPTRDFALKGNLRIQRH-----GKVEP-----DWT 165
Db 52 VKNSTCLDDSDWIHPNLTTPSPK-----DLQIQLHFAHTQGGDLFFPAVHLEWT 99
QY 166 -----HKGMEVGT-----GYNRRWVQLSGGPFESFDLLPEA 196
Db 100 LQTDASILYLEGAELSVLQLNTNERLCVRFEFLSKLRHHRRW-----RFTFS----- 147
QY 197 RAIRVTISSGPEVSVRLCHOWALCEELSSPYDVQKTVSGGHTVLPYEFLLP----- 249
Db 148 ---HFVVDPOQEYEVTVHH-----LPRDIPDGNHOSKNEFLVDPCEHARM 190
QY 250 ---CLCIEASYLOEDTV-----RRKKCPQSWPEAYGSDFWKSVHFTDYSHQHTQWMA 299
Db 191 KVTTPCMSSGSLWDPNITVETLEAHQLRVSTLWNE-----STHYQILLT 235
QY 300 LTLRCPLKLEAALCQRHDWHTLCKDLPNATARESDGWYVLEKVDLHPQLCFKVPWFES-- 357
Db 236 ---SFP-HMENHSCFEH-MHHIPAPRPEEFHQRSNVTLTLRLNKGCCRHQVQIQFFSSC 290
QY 358 ----FGNSHVECPHOTGSLTSWNVSMDTQAQQLILHFSSRMHATFSAWSLPLGQDTL 413
Db 291 LNDCLRHSAIVSCPEM-----PDT 310
QY 414 VPPVTVSVQWRSQVQFAMKHLCPDVSYRHLGLLILALLLTLGLGVVLAITCRPSQG 473
Db 311 EP-----IPDYNPLWVYFETIGSILLVGSVIL-----LIVCMWNR--LAG 349
QY 474 PG-----PA-----RPVLLHAADESAQRRLVGAELALLRAALGGG 509
Db 350 PGSEKYSDDTKYTDGLPAADLIPPLPKPKVWIIYSADHPLYVDVVLKFAQFLLTAC--G 407
QY 510 RDVVDLWEGRHVARVGPPLWMAARTVAREQGTVLLWS-----GADLR- 555
Db 408 TEVALDLLEEQAISEAGVMTWVGROKQEVESNSKIIIVLCSRGTRAKWQALLGRGAPVRL 467
QY 556 -----PVSGPDPRAAPLIALHAAAPR-----LLLAYFSRLCAKGDIPPLRALPYRL 605
Db 468 RCDHGKPVG--DLFTAAMNMILPDFKRPACFGTYVVCYFSEVSCDGDVDFLFGAAPRYPL 525
QY 606 L 606
Db 526 M 526

RESULT 5

US-09-022-696-10
; Sequence 10, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle


```

QY 300 LTLRCPLKLEAALCQRHWHHTLCKDLPNATARESDGWYVLEKVDLHPQLCFKVPWFSS-- 357
Db 236 ---SFP-HMENHSCFEH-MHHIPAPRPEEPHQRSNVTLLRNKGGCRHQVQIQPFSSC 290
QY 358 -----FGNSSHVECPHOTGSLTSWNVSDMTQAQQLILHFSSRMHATFSAAWSLPGLGQDTL 413
Db 291 LNDCLRHSATVSCPEM----- 526 M 526
QY 414 VPPVTVSQVWRSDVQFAWKHLCPDVSRYHGLGLLLIALLALLTLGLGVVLAALTCRRPQSG 473
Db 311 EP-----IPDYMLPWYFVITGTSILLVGSVIL-----LIVCMTWR--LAG 349
QY 474 PG-----PA-----RPVLLHHAADSEAQRRLVGAELRAALGCGG 509
Db 350 PGSEKYSDDTKYTDGLPAADLIPPLPKRWYIISADHPLYVDVVLKFAQFLLTAC--G 407
QY 510 RDVIVDLWEGRHVARVGPPLWMAATRVAREQGTVLLWS-----GADLR- 555
Db 408 TEVALDLLEEQATSEAGVMTWVGROKQEMVESNSKIIVLCSRGTRAKWQALLGRGAPVRL 467
QY 556 -----PVSGPDPRAPLLALLHAAPRP-----LALLAYFSRLCAKGDIPPLRALPRYL 605
Db 468 RCDHGKPVG--DLFTAAMNMILPDFKRPACFGTYVVCYFSEVSCDGDVDPDLFGAAPRYPL 525
QY 606 L 606
Db 526 M 526

RESULT 7
US-09-022-253-10
; Sequence 10, Application US/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)

```

```

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-253-10

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```

Query Match 3.5%; Score 123; DB 3; Length 866;
Best Local Similarity 18.0%; Pred. No. 0.0029;
Matches 108; Conservative 74; Mismatches 183; Indels 236; Gaps 26;

QY 116 LRGSCLVVTCURRAITFPSPQTPTRDFALKGNLRIQRH-----GKYVFP-----DWT 165
Db 52 VKNSTCLDSDSIHPRNLTPSSPK-----DLQIQLHFAHTQGDLPFAVHEWT 99
QY 166 -----HKGMEVGT-----CYNRRWVQLSGSPSEFDLLPEA 196
Db 100 LQTDASILYLEGAELSVQLNLTNERLCVRFELSKLRHHHRW-----RFTFS----- 147
QY 197 RAIRVTIISGPEVSVYRLCHQWALECEELSPYDQKIVSGGHTVELPYEFLLP----- 249
Db 148 ---HFVDPDQOEYEVTVHH-----LPKPIPCDGNHQSKNFLVPDCEHARM 190
QY 250 ---CLCIEASYLQEDTV-----RRKKCPQSWPEAYGDFWKSVFHTDYVSQHTQMVMA 299
Db 191 KVTTCMSSGSLMDPNITVETLEAHQLRVSFLLWNE-----STHYQILLT 235
QY 300 LTLRCPLKLEAALCQRHWHHTLCKDLPNATARESDGWYVLEKVDLHPQLCFKVPWFSS-- 357
Db 236 ---SFP-HMENHSCFEH-MHHIPAPRPEEPHQRSNVTLLRNKGGCRHQVQIQPFSSC 290
QY 358 -----FGNSSHVECPHOTGSLTSWNVSDMTQAQQLILHFSSRMHATFSAAWSLPGLGQDTL 413
Db 291 LNDCLRHSATVSCPEM----- 526 M 526
QY 414 VPPVTVSQVWRSDVQFAWKHLCPDVSRYHGLGLLLIALLALLTLGLGVVLAALTCRRPQSG 473
Db 311 EP-----IPDYMLPWYFVITGTSILLVGSVIL-----LIVCMTWR--LAG 349
QY 474 PG-----PA-----RPVLLHHAADSEAQRRLVGAELRAALGCGG 509
Db 350 PGSEKYSDDTKYTDGLPAADLIPPLPKRWYIISADHPLYVDVVLKFAQFLLTAC--G 407
QY 510 RDVIVDLWEGRHVARVGPPLWMAATRVAREQGTVLLWS-----GADLR- 555
Db 408 TEVALDLLEEQATSEAGVMTWVGROKQEMVESNSKIIVLCSRGTRAKWQALLGRGAPVRL 467
QY 556 -----PVSGPDPRAPLLALLHAAPRP-----LALLAYFSRLCAKGDIPPLRALPRYL 605
Db 468 RCDHGKPVG--DLFTAAMNMILPDFKRPACFGTYVVCYFSEVSCDGDVDPDLFGAAPRYPL 525
QY 606 L 606
Db 526 M 526

RESULT 8
US-09-022-260-10
; Sequence 10, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA

```

Qy 556 -----PVSGDPDRAAPLALLHAARP-----LLLLAYFSRLCAKGDIPPLRALPRYL 605
Db 468 RCDHCKPVG--DLFTAMNMILPDKRPAFCGTYYVCFSEVSCDGDVDPDLFGAAPRPL 525
Qy 606 L 606
Db 526 M 526
RESULT 9
US-09-022-259-10
; Sequence 10, Application US/09022259
; Patent No. 6191104
; GENERAL INFORMATION:
; APPLICANT: Yao Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: NO. 6191104el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-259-10

Qy 116 LRGSCCLVVTCLRRATFPSPPTSPTRDFALKGNLRIQRH-----GRVFP-----DWT 165
Db 52 VKNSTCLDDSDWIHPNLTTPSSPK-----DLQIQLHFAHTQQGDLFPVAHIEWT 99
Qy 166 -----HKGMEVGT-----GYNNRWVQLSGGPEFSFDLLPEA 196
Db 100 LOTDASILYLEGAELSVLQNTNERLCVRFELSKLRHHRRW-----RTFS----- 147
Qy 197 RAIKVTISSGPEVSVRLCHOWALECEELSSPDYDQKIVSGHVTPELFLP----- 249
Db 148 ---HFVVDPDQOEYEVVHH-----LPKPIPDGDPNHQSKNPLVDPCEHARM 190
Qy 250 ---CLCTEASVLOEDTV-----RRKKCPQSPWEAYGSDFWKSVHFTDYSQHTQVMA 299
Db 191 KVTTPCMSSGSLNDPNTVETLEAHQLRVSTLWNE-----STHYQILLT 235
Qy 300 LTLRCLPLKLEALCORHDWHTLCKDLPNATARESDGWYVLEKVDLHQLCFKVPQWPS-- 357
Db 236 ---SFP-HMENHSCFEH-MHHIPAPRPEEFHQRSNVTLTLRNLKGCRCRHQVQIQPFSSC 290
Qy 358 ---FGNSSHVCEPHQCSLTSNVSMDTQAOQLLHFSSRMHATFSAANSLPCLGQDTL 413
Db 291 LNDCLRHSATVSCPEM-----PDTP 310
Qy 414 VPPVTVSQVWKSVDQFAWKHLCPDVSYRHLGLLILALLALLTLGLGVLTALTCRRPQSG 473
Db 311 EP-----IPDYMPLVWVWFITGISILLVGSVIL-----LIVCMTWLW--LAG 349
Qy 474 PG-----PA-----RPVLLHHAADSEARQLVGLAELRAALGGG 509
Db 350 PGSEKYSDDTKYTDGLPAADLIPPLPKRVWIIYSADHPPLYVDVLKFAQLLTAAC--G 407
Qy 510 RDVVDLWEGRHVARVGPLPLWLAARTVAREQGTVLVLLWS-----GADLR-- 555
Db 408 TEVALDLLLEQAISAGVMTWVGROKQEMVESNKIIIVLCRSGTRAKWQALLRGAPVRL 467
Query Match 3.5%; Score 123; DB 3; Length 866;
Best Local Similarity 18.0%; Pred. No. 0.0029;
Matches 108; Conservative 74; Mismatches 183; Indels 236; Gaps 26;
Qy 116 LRGSCCLVVTCLRRATFPSPPTSPTRDFALKGNLRIQRH-----GRVFP-----DWT 165
Db 52 VKNSTCLDDSDWIHPNLTTPSSPK-----DLQIQLHFAHTQQGDLFPVAHIEWT 99
Qy 166 -----HKGMEVGT-----GYNNRWVQLSGGPEFSFDLLPEA 196
Db 100 LOTDASILYLEGAELSVLQNTNERLCVRFELSKLRHHRRW-----RTFS----- 147
Qy 197 RAIKVTISSGPEVSVRLCHOWALECEELSSPDYDQKIVSGHVTPELFLP----- 249
Db 148 ---HFVVDPDQOEYEVVHH-----LPKPIPDGDPNHQSKNPLVDPCEHARM 190
Qy 250 ---CLCTEASVLOEDTV-----RRKKCPQSPWEAYGSDFWKSVHFTDYSQHTQVMA 299
Db 191 KVTTPCMSSGSLNDPNTVETLEAHQLRVSTLWNE-----STHYQILLT 235
Qy 300 LTLRCLPLKLEALCORHDWHTLCKDLPNATARESDGWYVLEKVDLHQLCFKVPQWPS-- 357
Db 236 ---SFP-HMENHSCFEH-MHHIPAPRPEEFHQRSNVTLTLRNLKGCRCRHQVQIQPFSSC 290
Qy 358 ---FGNSSHVCEPHQCSLTSNVSMDTQAOQLLHFSSRMHATFSAANSLPCLGQDTL 413
Db 291 LNDCLRHSATVSCPEM-----PDTP 310
Qy 414 VPPVTVSQVWKSVDQFAWKHLCPDVSYRHLGLLILALLALLTLGLGVLTALTCRRPQSG 473
Db 311 EP-----IPDYMPLVWVWFITGISILLVGSVIL-----LIVCMTWLW--LAG 349
Qy 474 PG-----PA-----RPVLLHHAADSEARQLVGLAELRAALGGG 509
Db 350 PGSEKYSDDTKYTDGLPAADLIPPLPKRVWIIYSADHPPLYVDVLKFAQLLTAAC--G 407
Qy 510 RDVVDLWEGRHVARVGPLPLWLAARTVAREQGTVLVLLWS-----GADLR-- 555
Db 408 TEVALDLLLEQAISAGVMTWVGROKQEMVESNKIIIVLCRSGTRAKWQALLRGAPVRL 467

QY 250 ---CLCIEASYLQEDTV-----RRKKCPFQSWPEAYGSDFWKSVHFTDYSOHTQWMA 299
Db 191 KVTTPCMSSGSLWDPNITVETLEAHQLRVSTLWNE-----STHYQILLT 235
QY 300 LTLRCPLKLEAALCQRHDWHTLCKDLPNATARESDGWYVLEKVDLHPQLCFKVPWFSS-- 357
Db 236 ---SFP-HMENHSCFEH-MHHIPAPRPEFHQRSNVTLTLRLNKGCCRHQVQIQPFSSC 290
QY 358 ---FGNSHVECPHOTGSLTSWNVSMDTQAQQLILHFSSRHATFSAWSLPLGQDTL 413
Db 291 LNDCLRHSATVSCPEM-----PDTP 310
QY 414 VPPVYTVSQWRSQVDFAMKHLCPDVSRYHLGLLALLLALLLGLVVLALTCRRPQSG 473
Db 311 EP-----IPDYMPLWVYFITGISILLVGSVIL-----LIVCMTWR--LAG 349
QY 474 PG-----PA-----RPVLLHAADEAQRRLVGLAELRAALGGG 509
Db 350 PGSEKYSDDTKYTDGLPAADLIPPLKPRKVMIIYSADHPLYVDVVLKFAQFLLTAC--G 407
QY 510 RDVIVDLWEGRHVARVGPLWLAARTVAREQGTVLLWS-----GADLR- 555
Db 408 TEVALDLLEEQAISEAGVMTWVGROKQEMVESNSKIIIVLCRGTAKWQALLGRGAPVRL 467
QY 556 ---PVSGDPDPRAPLALLHAAAPR-----LLLAYFSRLCAKGDIPPLRALPRYL 605
Db 468 RCDHGKPVG--DLFTAAMNMLPDKRPAFCFTYVVCYFSEVSCDGDVDFLFGAAPRYL 525
QY 606 L 606
Db 526 M 526

RESULT 10

US-09-022-257-10
; Sequence 10, Application US/09022257
; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-257-10

Query Match 3.5%; Score 123; DB 4; Length 866;
Best Local Similarity 18.0%; Pred. No. 0.0029;
Matches 108; Conservative 74; Mismatches 183; Indels 236; Gaps 26;

QY 116 LRGSCCLVVTCLRRATFPSPQPTSPTRDFALGPNLRIQRH-----GKVPF--DWT 165
Db 52 VKNSTCLDDSWIHPNLTTPSSPK-----DLQIQLEHAHTQGGDLFPVAHIEWT 99
QY 166 -----HKGMEVGT-----GYNRRWVQLSGGPEFSFDLLPEA 196
Db 100 LQTDASTILYLEGAELSVLQLTNRLCVRFEFLSKLRHHHRW-----RFTFS-- 147
QY 197 RAIRVTISSGPEVSVRLCHQWALECELSSPDYQKIVSGGHTVLPYFELLP----- 249
Db 148 ---HFVVDPPQEEYEVVHH-----LPKPIPDGDPNHQSKNLFVLPDCEHARM 190
QY 250 ---CLCIEASYLQEDTV-----RRKKCPFQSWPEAYGSDFWKSVHFTDYSOHTQWMA 299
Db 191 KVTTPCMSSGSLWDPNITVETLEAHQLRVSTLWNE-----STHYQILLT 235
QY 300 LTLRCPLKLEAALCQRHDWHTLCKDLPNATARESDGWYVLEKVDLHPQLCFKVPWFSS-- 357
Db 236 ---SFP-HMENHSCFEH-MHHIPAPRPEFHQRSNVTLTLRLNKGCCRHQVQIQPFSSC 290
QY 358 ---FGNSHVECPHOTGSLTSWNVSMDTQAQQLILHFSSRHATFSAWSLPLGQDTL 413
Db 291 LNDCLRHSATVSCPEM-----PDTP 310
QY 414 VPPVYTVSQWRSQVDFAMKHLCPDVSRYHLGLLALLLALLLGLVVLALTCRRPQSG 473
Db 311 EP-----IPDYMPLWVYFITGISILLVGSVIL-----LIVCMTWR--LAG 349
QY 474 PG-----PA-----RPVLLHAADEAQRRLVGLAELRAALGGG 509
Db 350 PGSEKYSDDTKYTDGLPAADLIPPLKPRKVMIIYSADHPLYVDVVLKFAQFLLTAC--G 407
QY 510 RDVIVDLWEGRHVARVGPLWLAARTVAREQGTVLLWS-----GADLR- 555
Db 408 TEVALDLLEEQAISEAGVMTWVGROKQEMVESNSKIIIVLCRGTAKWQALLGRGAPVRL 467
QY 556 ---PVSGDPDPRAPLALLHAAAPR-----LLLAYFSRLCAKGDIPPLRALPRYL 605
Db 468 RCDHGKPVG--DLFTAAMNMLPDKRPAFCFTYVVCYFSEVSCDGDVDFLFGAAPRYL 525
QY 606 L 606
Db 526 M 526

RESULT 11

US-08-620-694A-2
; Sequence 2, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; STREET: 51 University Street
; CITY: Seattle

STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER: Apple Power Macintosh
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-620-694A-2

338 VIVLIICMTWRLSGADQEKHDDSKINGILPVADLTPTPLPRKRWIVYSADHPLVVEV 397
496 GALAEILRAALGGGRDVIDLWEGRHVARVGLPWLWAAARTRVAREQGVLLLLWS---GA 552
398 LKFAQLITAC--GTEVALDLEEQVISEVGVWTVSRQKQEMVESKIIILCSRGTOA 455
553 DLRPVSG-----PDRAAPLALLHAAPRP-----ILLAYFSLCAKGD 592
456 KWKAILGMAEPVQLRCDHWKPGADLFTAAMNMLPDKRPACFGTVVVCYFSGICSERD 515
593 IPPPLRALPRYRL 606
516 VPDLFNITSRYPLM 529

RESULT 12
US-09-022-255-2
Sequence 2, Application US/09022255
Patent No. 6072033
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-255-2

Query Match 3.5%; Score 121.5; DB 2; Length 864;
Best Local Similarity 17.5%; Pred. No. 0.0041;
Matches 118; Conservative 97; Mismatches 182; Indels 277; Gaps 33;
46 VLPISLAAPGGSSPSQSLGVCESGTPA-VCA--SICCOVAQVFNAGSSTSCNRNPKSLP 102
20 LLLNLVAP-GRASPRLL-----DFPAPVCAQEGLSCKVKN--STCLDDSWI-HPKNLT 69
103 HSSSIGDTRCQHLRGSCCLVVTCLRRAITFPSPPTSTPTDFALKGNPLRIQ--RHGKV 160
70 -----PSSPKNIYI-----NLSVSSSTQHGL 90
161 FP-----DWT-----HKGMEVGT-----GYNRVQVLSGGPE 187
91 VPLVHVEWTLQTDASILYLEGAEISVLQNTNERLCVKFQLSMLQHHKRW-----R 143
188 FSDLLPEARAIRVTISSGPEVSVRLCHQ-----WALECEELSSPYDVQ 231
144 FSGS-----HFVDPGQGEYEVTHLKPDPDGNPHKSLIIFVPCDESKMKMTTS 195
232 KIVSG-----GHTVELPYEFLFLCLCEASYLOED-TVRRKKCPQSQWPEAYGSDFWKSV 285
196 CVSSGSLWDNIIVE-----TLDTQHLRVDFTLNNESTPYQVLLS----- 236
286 HFTDYSQHTQWVALTRCPKLEAALCORHDWHTLCKDLPNATARESOGWYVLEKVDLH 345
237 -FSDSENHSCFDVVKQIFAP-----RQEEFH-----QRANVTFTLSKPHWC 276
346 POLCFKVPWFSS-----FGNSSHVECPHQTGSLTSWNVSMDTQAQQLILHFSRHMATF 399
277 CHHVVQVQPFSSCLNCLRHAVTVPCP----- 304
400 SAAWSLPLGQDITLVP-PVYTVSQVRSQVDFANKHLLCPDVSYRHLGLL-ILALLALT 457
305 -----VISNTVPKPVADYIPLW-----VYGLITLAIILVGS 337
458 LLGVVLAITCR-----RPSQG-----PGARP--VLLLHAADSEARRLV 495

Query Match 3.5%; Score 121.5; DB 3; Length 864;
Best Local Similarity 17.5%; Pred. No. 0.0041;
Matches 118; Conservative 97; Mismatches 182; Indels 277; Gaps 33;
46 VLPISLAAPGGSSPSQSLGVCESGTPA-VCA--SICCOVAQVFNAGSSTSCNRNPKSLP 102
20 LLLNLVAP-GRASPRLL-----DFPAPVCAQEGLSCKVKN--STCLDDSWI-HPKNLT 69
103 HSSSIGDTRCQHLRGSCCLVVTCLRRAITFPSPPTSTPTDFALKGNPLRIQ--RHGKV 160

Query Match 3.5%; Score 121.5; DB 3; Length 864;
Best Local Similarity 17.5%; Pred. No. 0.0041;
Matches 118; Conservative 97; Mismatches 182; Indels 277; Gaps 33;
46 VLPISLAAPGGSSPSQSLGVCESGTPA-VCA--SICCOVAQVFNAGSSTSCNRNPKSLP 102
20 LLLNLVAP-GRASPRLL-----DFPAPVCAQEGLSCKVKN--STCLDDSWI-HPKNLT 69
103 HSSSIGDTRCQHLRGSCCLVVTCLRRAITFPSPPTSTPTDFALKGNPLRIQ--RHGKV 160

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Db 70 -----PSSPKNIYI-----NLSSVSTQHGL 90
QY 161 FP-----DWT-----HKGMEVGT-----GYNRRWVQLSGGPE 187
Db 91 VPLHVEWTLDQDASILYLEGAELSVLQNTNRLNLCVKFQFLSLMLQHRKRW-----R 143
QY 188 FSDLLPEARAIKVTISSGPEVSVRLCHQ-----WALECEELSPYDVQ 231
Db 144 FSES-----HFVDPGQEVETVHLPKIPDGDPNHKSIIFFVPCDESKMKMTTS 195
QY 232 KIVSG-----GHTVELPYEFLPCLEASYLQED--TVRRKKCPQSPWEAYGSDFWKSV 285
Db 196 CVSSGSLWDPNITVE-----TLDQHLRVDFTLWNESTPYQVLLES-----236
QY 286 HFTDYSQHTQVMYALTRCPLKLEALCORHWHITLCKDLPNATARESDGHWYVLEKVDLH 345
Db 237 -FSDSENHSCFDVVKQIFAP-----RQEEFH-----QRANVTFTLSKFHWC 276
QY 346 POLCEKVPWF-----FGNSHVECPHOTGSLTSWNVSMDSMDTQAQQLILHFSSRMHATF 399
Db 277 CHHHVQVQPFSSCLNDCRLRHAVTVPCP-----304
QY 400 SAANSLPLGLGQDTLVP--PVYTVSQWRSDVOPAWKHLHLLCPDVSYRHLGLL--ILALLALT 457
Db 305 -----VISNTTPKPVADYIPLW-----VYGLITLAILLVGS 337
QY 458 LLGVVLALTCR-----RQSG-----PGPARP--VLLHHAADSEAQRRLV 495
Db 338 VIVLICHTWRLSGADQEKHDDSKINGILPVADLTTPPLRPRKVIWVYADHPLYEVV 397
QY 496 GALAEALLRAALGGGRDVIWDLMEGRHVARVGPPLMWARTRVAREQGTVLLLWS---GA 552
Db 398 LKFAQLITAC--GTEVALDLLEEQVISEVGVMTVWSRQKQEMVESNSKIILSRGTQA 455
QY 553 DLRPVSG-----PDRAAPLLALLHAAPR-----LALLAYFSRLCAKGD 592
Db 456 KWKAILGWAEPVQLRCDHKKPAGDLTAAMNMLPDKRPAFCGTYYVCYFSGICSERD 515
QY 593 IPPPLRALPRYRL 606
Db 516 VPDLFNITSRYPLM 529

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RESULT 13

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US-09-022-696-2
; Sequence 2, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fauslow, William
; TITLE OF INVENTION: No. 6072037e1 Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-696-2

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Query Match 3.5%; Score 121.5; DB 3; Length 864;
Best Local Similarity 17.5%; Pred. No. 0.0041;
Matches 118; Conservative 97; Mismatches 182; Indels 277; Gaps 33;

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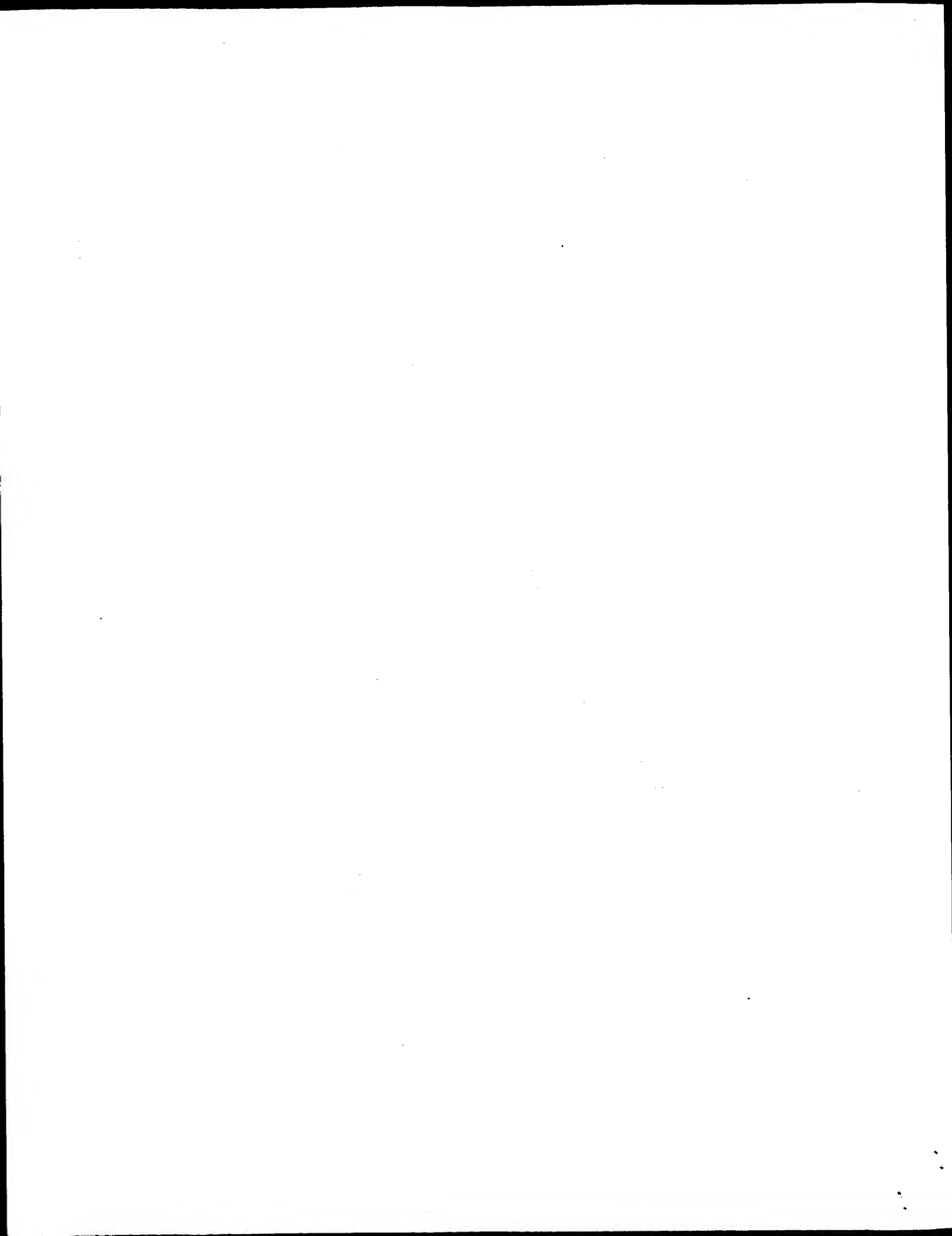
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QY 103 HSSISGTRCQHLRGSCCLVVTCLRRATFFSPPTSPTRDFALKGNLRIQ--RHGKV 160
Db 70 -----PSSPKNIYI-----NLSSVSTQHGL 90
QY 161 FP-----DWT-----HKGMEVGT-----GYNRRWVQLSGGPE 187
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QY 188 FSDLLPEARAIKVTISSGPEVSVRLCHQ-----WALECEELSPYDVQ 231
Db 144 FSES-----HFVDPGQEVETVHLPKIPDGDPNHKSIIFFVPCDESKMKMTTS 195
QY 232 KIVSG-----GHTVELPYEFLPCLEASYLQED--TVRRKKCPQSPWEAYGSDFWKSV 285
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QY 286 HFTDYSQHTQVMYALTRCPLKLEALCORHWHITLCKDLPNATARESDGHWYVLEKVDLH 345
Db 237 -FSDSENHSCFDVVKQIFAP-----RQEEFH-----QRANVTFTLSKFHWC 276
QY 346 POLCEKVPWF-----FGNSHVECPHOTGSLTSWNVSMDSMDTQAQQLILHFSSRMHATF 399
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Search completed: January 28, 2003, 09:31:17
Job time : 23 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 28, 2003, 09:30:38 : Search time 14 Seconds
(without alignments)
946.951 Million cell updates/sec

Title: US-09-863-818a-12
Perfect score: 3512
Sequence: 1 MGSSRLAALLPLILLIVIDL.....SRLECSRLREARLADLG 657

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

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2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2711	77.2	667	9	US-10-000-157-16
3	2711	77.2	667	9	US-09-816-744-16
4	2711	77.2	667	9	US-09-747-259-16
5	1108	31.5	226	10	US-09-893-737-328
6	313	8.9	638	10	US-09-899-471-5
7	312.5	8.9	674	10	US-09-899-471-2
8	304.5	8.7	692	10	US-09-899-471-8
9	299	8.5	705	9	US-09-874-503-14
10	299	8.5	705	9	US-10-000-157-14
11	299	8.5	705	9	US-10-063-547-162
12	299	8.5	705	9	US-09-816-744-14
13	299	8.5	705	9	US-09-747-259-14
14	299	8.5	705	9	US-10-174-590-598
15	299	8.5	705	9	US-10-176-758-598
16	299	8.5	705	9	US-10-063-616-162
17	299	8.5	705	9	US-10-175-737-598
18	299	8.5	705	12	US-10-006-867-162
19	299	8.5	705	12	US-10-052-586-598

20	153	4.4	204	9	US-09-949-842-25	Sequence 25, Appl
21	123	3.5	810	10	US-09-809-567-3	Sequence 3, Appl
22	123	3.5	866	10	US-09-778-971-9	Sequence 9, Appl
23	123	3.5	866	12	US-10-033-522-1	Sequence 1, Appl
24	114.5	3.3	635	9	US-10-099-895-33	Sequence 33, Appl
25	113.5	3.2	2854	8	US-08-424-5508-394	Sequence 394, App
26	102	2.9	576	10	US-09-931-087A-1	Sequence 1, Appl
27	102	2.9	576	10	US-09-931-087A-21	Sequence 21, Appl
28	102	2.9	576	10	US-09-931-087A-22	Sequence 22, Appl
29	101	2.9	576	10	US-09-931-087A-23	Sequence 23, Appl
30	101	2.9	781	10	US-09-860-868-2	Sequence 2, Appl
31	101	2.9	994	10	US-09-852-909-2	Sequence 2, Appl
32	101	2.9	1089	9	US-10-174-590-266	Sequence 266, App
33	101	2.9	1089	9	US-10-176-758-266	Sequence 266, App
34	101	2.9	1089	9	US-10-175-737-266	Sequence 266, App
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36	100	2.8	2862	10	US-09-743-659-5	Sequence 5, Appl
37	100	2.8	2864	10	US-09-743-659-2	Sequence 2, Appl
38	100	2.8	2865	10	US-09-742-659-6	Sequence 6, Appl
39	99.5	2.8	1168	9	US-09-935-868-24	Sequence 24, Appl
40	99	2.8	7257	9	US-10-014-717-5	Sequence 5, Appl
41	96.5	2.7	948	10	US-09-897-699-2	Sequence 7, Appl
42	95.5	2.7	954	9	US-09-944-413-7	Sequence 7, Appl
43	95.5	2.7	954	9	US-09-944-403-7	Sequence 7, Appl
44	95.5	2.7	954	9	US-09-944-896-7	Sequence 7, Appl
45	95.5	2.7	954	9	US-09-944-944-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

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; Sequence 16, Application US/09874503
; Patent No. US20020177188A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah G.
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovasinik, Melissa A.
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P3(US)
; CURRENT APPLICATION NUMBER: US/09/874,503
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/244,072
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/213,807
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/138,387

;; PRIOR FILING DATE: 1999-06-09
;; PRIOR APPLICATION NUMBER: US 60/134,287
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US 60/131,022
;; PRIOR FILING DATE: 1999-04-26
;; PRIOR APPLICATION NUMBER: US 60/130,232
;; PRIOR FILING DATE: 1999-04-21
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;; PRIOR FILING DATE: 2001-05-10
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;; PRIOR FILING DATE: 2001-05-20
;; PRIOR APPLICATION NUMBER: US 09/816,744
;; PRIOR FILING DATE: 2001-03-22
;; PRIOR APPLICATION NUMBER: US 09/747,259
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: US 09/644,848
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;; PRIOR APPLICATION NUMBER: US 09/380,138
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: US 09/311,832
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US PCT/US01/06520
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: US PCT/US00/34956
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: US PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
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;; PRIOR FILING DATE: 2000-11-10
;; PRIOR APPLICATION NUMBER: US PCT/US00/23328
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;; PRIOR APPLICATION NUMBER: US PCT/US00/15264
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;; PRIOR APPLICATION NUMBER: US PCT/US00/07532
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;; PRIOR APPLICATION NUMBER: US PCT/US00/04341
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;; PRIOR FILING DATE: 1999-12-30
;; PRIOR APPLICATION NUMBER: US PCT/US99/10733
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US PCT/US99/05028
;; PRIOR FILING DATE: 1999-03-08
;; NUMBER OF SEQ ID NOS: 39
;; SEQ ID NO 16
;; LENGTH: 667
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-874-503-16

Query Match 77.2%; Score 2711; DB 9; Length 667;
Best Local Similarity 77.5%; Pred. No. 1.1e-215;
Matches 548; Conservative 15; Mismatches 54; Indels 90; Gaps 11;
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QY 117 ---RGSCCLVVTCLRRATF-----PSPQTS---PTRDFALKGNLRIQRHGKVFDP 163

Db 90 GLQGLFHLLVQKSKSSTFKFYRRHKMPAPQAKRLPRHLSEKSHIIPS-----PD 144
QY 164 WTHKGM-----EVGTGYNRRWQLSGGPESFDLLPEARAIRVTISSGPEVSRL 213
Db 145 ISHKLRSKRTQPSDPTWESLPRDSQRGGPESFDLLPEARAIRVTISSGPEVSRL 204
QY 214 CHOWALECEELSSPYDVQKIVSGGHTVELPEFLPLCLCIEASYLOEDTVRRKKCPQSW 273
Db 205 CHOWALECEELSSPYDVQKIVSGGHTVELPEFLPLCLCIEASYLOEDTVRRKKCPQSW 264
QY 274 PEAYGDFWKSVDYTSOHTQVMYALTLCRPLKLEALCORHDMHTLCKDLNATARES 333
Db 265 PEAYGDFWKSVDYTSOHTQVMYALTLCRPLKLEALCORHDMHTLCKDLNATARES 324
QY 334 DGWVLEKVDLHPOLCFKVPWFSGNSSHVECPHQTGSLTSWNVSMDTQAQQLILHFSS 393
Db 325 DGWVLEKVDLHPOLCFK-----FSGNSSHVECPHQTGSLTSWNVSMDTQAQQLILHFSS 380
QY 394 RMHATFSAWSLPLGLGQDTLVPVTVTSQ-----VVRSDVQF 430
Db 381 RMHATFSAWSLPLGLGQDTLVPVTVTSQARGSPVSLDLIIPFLRPGCCVLVNRSDVQF 440
QY 431 AWKHLPCDVSRYHGLLILALLLGLVLTALTCRRPQSGPGPARPVLLHHAADSEA 490
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QY 491 QRRVLGALAEALLRAALGGRDVIVDLWEGRHVARVGPLWLAARTVARBQGTVLLWS 550
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QY 611 RLLRALDARPAEATSWRGLGARQRQRSLCRLSEKLEBEAARLADLG 657
Db 621 RLLRALDARPAEATSWRGLGARQRQRSLCRLSEKLEBEAARLADLG 667

RESULT 2
US-10-000-157-16
; Sequence 16, Application US/10000157
; Publication No. US20020182673A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul L.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovasinik, Melissa.
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P4(US)
; CURRENT APPLICATION NUMBER: US/10/000,157
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/130232
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;; PRIOR APPLICATION NUMBER: PCT/US01/21066
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;; SEQ ID NO 16
;; LENGTH: 667
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;; ORGANISM: Homo Sapien
US-10-000-157-16

Query Match 77.28; Score 2711; DB 9; Length 667;

Best Local Similarity 77.5%; Pred. No. 1.1e-215;

Matches 548; Conservative 15; Mismatches 54; Indels 90; Gaps 11;

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DB 145 ISHGLRSKRTQSDPETWESLRLDSQRGGPEFSDLLPEARAIRVTISSGPEVSRL 204
QY 214 CHOWALECEELSSPDYQKIVSGGHTVELPYEFLLPCLCTEASYLQEDTVRRKKCPQSW 273
DB 205 CHOWALECEELSSPDYQKIVSGGHTVELPYEFLLPCLCTEASYLQEDTVRRKKCPQSW 264
QY 274 PEAYGDFWKSVIHFTDYSQHTQVMALTRCPLKLEALCORHDWHTLCKDLNPATRES 333
DB 265 PEAYGDFWKSVIHFTDYSQHTQVMALTRCPLKLEALCORHDWHTLCKDLNPATRES 324
QY 334 DGWTVLEKVDLHPOLCFKVPWFSGNSHVCEPHOTGSLTSNNVSMDOCAQOLILHFS 393
DB 325 DGWTVLEKVDLHPOLCFK----FSGNSHVCEPHOTGSLTSNNVSMDOCAQOLILHFS 380
QY 394 RMHATFSAANSLPGLQDITLVPVYTVSQ-----VMSDVQF 430
DB 381 RMHATFSAANSLPGLQDITLVPVYTVSQARSSPSVSLDLIIPFLRPGCCVLVMSDVQF 440
QY 431 AWKHLICPDVSYRHLGLLIIALLALLTLGLVVALTCRRPQSGPGPARVLLLHAADSEA 490
DB 441 AWKHLICPDVSYRHLGLLIIALLALLTLGLVVALTCRRPQSGPGPARVLLLHAADSEA 500
QY 491 QRLVGLALAEALLRAALGGGRDVIVDLWEGRHVARVGPLWMLWAARTVAREQCTVLLLWS 550
DB 501 QRLVGLALAEALLRAALGGGRDVIVDLWEGRHVARVGPLWMLWAARTVAREQCTVLLLWS 560
QY 551 GADLRVSGPDPRAAPLALLHAAPRLLLLAYFSRLCAKGDIPPLRALPRYLLRLDLP 610
DB 561 GADLRVSGPDPRAAPLALLHAAPRLLLLAYFSRLCAKGDIPPLRALPRYLLRLDLP 620
QY 611 RLLRALDARFAEATSWGLGARQSRQSLRLELCRLEREAAARLADLG 657
DB 621 RLLRALDARFAEATSWGLGARQSRQSLRLELCRLEREAAARLADLG 667

RESULT 3

US-09-816-744-16

; Sequence 16, Application US/09816744

; Publication No. US20030003546A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Jian

```
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P2(US)
; CURRENT APPLICATION NUMBER: US/09/816,744
; PRIOR FILING DATE: 2001-03-22
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 16
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-816-744-16

Query Match 77.2%; Score 2711; DB 9; Length 667;
Best Local Similarity 77.5%; Pred. No. 1.le-215;
Matches 548; Conservative 15; Mismatches 54; Indels 90; Gaps 11;

QY 1 MGSSRLAALLPLLLIVDLSAGTGFPHLPWNTROPLASHTVLPISLAAPGGPSSP 60
DB 1 MGSSRLAALLPLLLIVDLSAGTGFPHLPWNTROPLASHTD----- 45
QY 61 QSLGVCESTVPVAVCASICQVAVFNGASSTWCNPKSLPHSSISIGTTRCOHLL---- 116
DB 46 -----DSFTGSSAYIPCRTWAL--FSTRKPCW---VRVWHCSR---CLCQHLLSGS 89
QY 117 ---RSGCCLVVTCLRAITF-----PSPQTS--PTRDFALGPNLRIGRHGKVPFD 163
DB 90 GLOGLFHLVLVOKSKSTFKFYRRHKMPAPAKRKLPRRHLSKSHLSIPS-----PD 144
QY 164 WTHKGM-----EVGTGYNRRWVQLSGGPFESFDLLPEARAIKVTISSGPEVSVRL 213
DB 145 ISHKLGRSKRTQPSDPTWESLPRLDSQRHGPGPFESFDLLPEARAIKVTISSGPEVSVRL 204
QY 214 CHOWALECEELSSPYDVQKIVSGGHTVELPYEFLPCICIEASYLOEDTVRRKKCPFSQW 273
DB 205 CHOWALECEELSSPYDVQKIVSGGHTVELPYEFLPCICIEASYLOEDTVRRKKCPFSQW 264
QY 274 PEAYGDFWKSVMHFTDYSOHTQVMWALTURCPKLEAALCORHWHITLCKLPNATARES 333
DB 265 PEAYGDFWKSVMHFTDYSOHTQVMWALTURCPKLEAALCORHWHITLCKLPNATARES 324
QY 334 DGWYVLEKVDLHPQLCFKVPWFSGNSHVECPHQGTSLTSWNYSMDTQAOQLILHFSS 393
DB 325 DGWYVLEKVDLHPQLCFK---FSGNSHVECPHQGTSLTSWNYSMDTQAOQLILHFSS 380
QY 394 RMHATSAWSLPGICQDILVPPVTVSQ-----VWRSQVQF 430
DB 381 RMHATSAWSLPGICQDILVPPVTVSQ-----VWRSQVQF 440
QY 431 AKWHLLCPDVSYSRHLLILALILTLGVVLTLCRRPQSGPGPARPVLLHAADSEA 490
DB 441 AKWHLLCPDVSYSRHLLILALILTLGVVLTLCRRPQSGPGPARPVLLHAADSEA 500
QY 491 QRLVGALAEALLRAALGGGRDVIDLWEGRHVARVGPPLPWLAARTVAREOGTVLLIWS 550
DB 501 QRLVGALAEALLRAALGGGRDVIDLWEGRHVARVGPPLPWLAARTVAREOGTVLLIWS 560
QY 551 GADLRVSGDPDPAAPLLALLHAAPRPLLLAYFSLCAKAGDIPPLRALPRYLLRLDLP 610
DB 561 GADLRVSGDPDPAAPLLALLHAAPRPLLLAYFSLCAKAGDIPPLRALPRYLLRLDLP 620
QY 611 RLLRALDARPFAPATSWGRLGARQRRORSLCRLCSRLEREARLADLG 657
DB 621 RLLRALDARPFAPATSWGRLGARQRRORSLCRLCSRLEREARLADLG 667

RESULT 4
US-09-747-259-16
; Sequence 16, Application US/09747259
; Publication No. US20030008815A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 16
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-747-259-16

Query Match 77.2%; Score 2711; DB 9; Length 667;
```

Best Local Similarity 77.5%; Pred. No. 1.1e-215;
Matches 548; Conservative 15; Mismatches 54; Indels 90; Gaps 11;

QY 1 MGSRRLAALLPLLLIIVIDLSDSAGIGFRHLPHWNTCRPLASHTVPLPISLAAPGGPSSP 60
DB 1 MGSRRLAALLPLLLIIVIDLSDSAGIGFRHLPHWNTCRPLASHTD-----45

QY 61 QSLGVCBSGRVPAVCASICQVAFNGASSTWCNRPKSLPHSSSIGDTRCOHLL---116
DB 46 -----DSFTGSSAIPCRTWAL--FSTKPKC-----VRWHCNR---CLCOHLLSGGS 89

QY 117 ---RGSCCLVVTCLURRAITP-----PSPQTS---PTRDFALKGNLRIQRHGVFPD 163
DB 90 GLQGLPHLLVQKSKSSTFKFYRRHKMPAPAKRLPRRHLSEKSHHISIP-----PD 144

QY 164 WTHKGM-----BVGTYGNRWVQLSGGPEFSDLLPEARAIKRTVISSGPEVSRL 213
DB 145 ISHGLRSKRTQSDPTWESLPLDSQRHGGEFSDLLPEARAIKRTVISSGPEVSRL 204

QY 214 CHOWALECEELSSPDYQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPQSW 273
DB 205 CHOWALECEELSSPDYQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPQSW 264

QY 274 PEAYGDFWKSVMFTDYSQHTQVMVMAITLRCPLKLEAALCORHDWHTLCKDLPNATARES 333
DB 265 PEAYGDFWKSVMFTDYSQHTQVMVMAITLRCPLKLEAALCORHDWHTLCKDLPNATARES 324

QY 334 DGWYVLEKVDLHPOLCFKVPWFSGNSSHVECPHOTGSLTSNNVSMDTQAQOLILHFS 393
DB 325 DGWYVLEKVDLHPOLCFK-----FSGNSSHVECPHOTGSLTSNNVSMDTQAQOLILHFS 380

QY 394 RHATFSAWLSPLGLGODTLVPPVYVSQ-----VWRSDDVOF 430
DB 381 RHATFSAWLSPLGLGODTLVPPVYVSQARGSSPVSLDIIIPFLPGCCVLWRSDDVOF 440

QY 431 AKWHLCPDVSYRHGLLIILALITLLGVVLTALTCRRPQSGPGPARPVLLHAADSEA 490
DB 441 AKWHLCPDVSYRHGLLIILALITLLGVVLTALTCRRPQSGPGPARPVLLHAADSEA 500

QY 491 QRLVAGALAEALLRAALGGGRDVTDLWEGRHVARVGPPLWMAARTVAREQGTVLLWS 550
DB 501 QRLVAGALAEALLRAALGGGRDVTDLWEGRHVARVGPPLWMAARTVAREQGTVLLWS 560

QY 551 GADLRVSGDPDRAAPLLALLHAAPRLLLAYFSLCAKGDIPPLRALPRYLLRLDLP 610
DB 561 GADLRVSGDPDRAAPLLALLHAAPRLLLAYFSLCAKGDIPPLRALPRYLLRLDLP 620

QY 611 RLRLADARPFAEATSWGLRGARQRQSRLELCSRLEREAAALADLG 657
DB 621 RLRLADARPFAEATSWGLRGARQRQSRLELCSRLEREAAALADLG 667

RESULT 5
US-09-893-737-328
; Sequence 328, Application US/09893737
; Patent No. US20020110855A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
; FILE REFERENCE: 00-41
; CURRENT APPLICATION NUMBER: US/09/893,737
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 328
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-737-328

Query Match 31.5%; Score 1108; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.3e-84;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 440 VSYRHGLLITALLALLTLLGVVLTALTCRRPQSGPGPARPVLLHAADSEAQRRLVGALA 499
DB 9 VSYRHGLLITALLALLTLLGVVLTALTCRRPQSGPGPARPVLLHAADSEAQRRLVGALA 68

QY 500 ELLRALGGRDVTVDLWEGRHVARVGPPLWMAARTVAREQGTVLLWSGADLRPVSG 559
DB 69 ELLRALGGRDVTVDLWEGRHVARVGPPLWMAARTVAREQGTVLLWSGADLRPVSG 128

QY 560 PDPRAAPLLALLHAAPRLLLAYFSLCAKGDIPPLRALPRYLLRLDLPRLALDAR 619
DB 129 PDPRAAPLLALLHAAPRLLLAYFSLCAKGDIPPLRALPRYLLRLDLPRLALDAR 188

QY 620 PFAEATSWGLRGARQRQSRLELCSRLEREAAALADLG 657
DB 189 PFAEATSWGLRGARQRQSRLELCSRLEREAAALADLG 226

RESULT 6
US-09-899-471-5
; Sequence 5, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 698
; TYPE: PRT
; ORGANISM: mouse
US-09-899-471-5

Query Match 8.9%; Score 313; DB 10; Length 698;
Best Local Similarity 25.1%; Pred. No. 7.3e-18;
Matches 180; Conservative 77; Mismatches 291; Indels 168; Gaps 34;

QY 32 PHWNTCRPLASHTV-----LPTSL-AARGPSSPQSLGV-----CESGTVPACVASI 78
DB 27 PDDTARCSLGLSCHLWDGVLCLPGSLQSAPEGLVLPTRLOTELVLRCPQKT---DCA-- 81

QY 79 CQVAVQVFNAGASSTWCNRPKSLPHSSSIGDTR-----CQHLRGSCCLVVTCLRRATF 133
DB 82 -LRVRVVVHLAVHGHWAPEAGKSDSELQESRNASLQAQVVLFSQAYPIARCALLEVQV 140

QY 134 PS-----PPQTSPTDRF-----ALKGNLRIQRHGK-----VFPDWTGHKMEVGTG 174
DB 141 PADLVQPGQSVGSVAFDCFEASLGAEVQIWSYTKPRYKELNLTAQLPDC--RGLEVRDS 198

QY 175 YNRRWV-----OLSGGPEFSFDL-----LPEARAIKRTVISSGPEVSRL 213
DB 199 IQSCWVLPWLVNSTDGDNVLLTLDVSEEDFSFLYLRPVDA-----L 242

QY 214 CHOWALECEELSSPDYQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPQSW 273
DB 243 KSLW-----YKNLTGQNTLNTDLVPLCLCQVLSLEPDSERVEFCPRD 289

QY 274 PEAYGDFWKSVMFTDYSQHTQVMVMAITLRCPLKLEAALCORHDWHTLCKDLP-----PN 327
DB 290 PCAH-RNLW---HIALRLVSPGVQWQLDAPCCLPGKVTLCWQADPQSPQCLVPPVPQKN 345

QY 328 ATARESDGWYVLEKVDLHPOLCFKVPWFSGNSSHVECPHOTGSLTSNNVSMDT-QAQQ 386
DB 346 ATVNEPQDF---QLVAGHPNLCVQVSTW-----EKVOL-----OACSWADSLGPFKDDM 391

QY 387 LILHFSRRMHTAF-----SAAWSLPG-----LGODTLVP-PVYTVSQVWRS-DVQF 430
DB 387 LILHFSRRMHTAF-----SAAWSLPG-----LGODTLVP-PVYTVSQVWRS-DVQF 430

Db 392 LLVEMKTLGNTSVCALEPGSGCTPLPSMASTRALGEBELLQDFRSHQCMQWLNDDNMGS 451
 QY 431 AKHLLCPDVSYRHG--LLIALLALLLLGWVLTALTCRRQSGGPGPARPVLLLHADS 488
 Db 452 LW---ACPMCKYIHRRWLVWVLAACLLAAALFFLLKKDKRKAAG--SRTALLLHSDG 507
 QY 489 EAQRRLVGALELLRAALGGGRDVIIVDLWEGRHRVARVGLPWLWAARTVAREQGTVLIL 548
 Db 508 AGYERLVGALASLSOM---PLRVAVDLWSRRLSAHGALAFHHRRLILQGGVVILL 564
 QY 549 WSGA-----DLRPVS-GDPRAAPLLA-----LLHAAPRPLLLLAYFRLCAKGI 593
 Db 565 FSPAAVAQCOOWLQLOQVTEPGPHDALAAMLSVLPDFLOGRATGRYGVYFDGLLHPDSV 624
 QY 594 PPLRALPRYRLRLDPLRLRALDARPAFAEATSWGLGARQRR----QSRLELCS 644
 Db 625 PSPFRVAPLSLTQLPFAFLDALOG---GCSTSGRPAADRVVTOALRSALDSCT 677

RESULT 7

US-09-899-471-2
 ; Sequence 2, Application US/09899471
 ; Patent No. US20020146763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gao, Zeren
 ; TITLE OF INVENTION: Murine Cytokine Receptor
 ; FILE REFERENCE: 00-46
 ; CURRENT APPLICATION NUMBER: US/09/899,471
 ; CURRENT FILING DATE: 2001-07-05
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 674
 ; TYPE: PRT
 ; ORGANISM: mouse
 US-09-899-471-2

Query Match 8.9%; Score 312.5; DB 10; Length 674;
 Best Local Similarity 25.3%; Pred. No. 7.7e-18;
 Matches 171; Conservative 65; Mismatches 276; Indels 165; Gaps 31;
 QY 96 RNP--KSLPHSSSIGDT-RQ-----HLRGSCCLVVTCLRRRAITFPSPQTSPTPR--D 144
 Db 14 RNPVVSLERLMEPDQTARCSGLSCHLWDGD---VLCPLGSLQAPGVLPVTPRLQTE 69
 QY 145 FALKGP-----NLRQRHGKVPDWT---HKGMEVGTGYNRRWVQLSGGPEFSDLLP 194
 Db 70 LVURCPQKTDCALRVVRVHLAVHGHWAEPPEAGKSDSELSQESRNASLQAOVVLSQAYP 129
 QY 195 EARAIRVTI-----SSGPEVSRYRLCHOWA-----WSYTKPRYQKELNLT 184
 Db 130 IARCALLEVQVPADLVQPGSGVSGSAVDFDCFEASLGAEVQI-----WSYTKPRYQKELNLT 184
 QY 219 -----LECEELSSPYDVQ-----KIVSGGHTVELPYEFLLPCLC 252
 Db 185 QQLPDGDNVLITLDVSEQDFSELLYLRVPDALKSLWKNTITGPQNTITLHFDLPCLC 244
 QY 253 IEASYLQEDTVRRKCKPQFQSWPBAYGDFWKSVFHTDYSOHTOMVVALTLRCPKLLEAAL 312
 Db 245 IQWLSPEPDSERVEFCFPREDPGAH--RNLW---HIARLRVLSGVWQLDAPCCLPKKVTL 300
 QY 313 QRIDHWTLCCKDL-----PNATARESDGWVLEKVDLHDLQPCFKVQPFQSWGSHVEFC 366
 Db 301 CWQAPDQSPCQPLVPVPVQPNATVNEPDF---QLVAGHPNLCVQVSTW-----EKVQL 351
 QY 367 PHQTGSLTSNNVMDT--QAQOLILHFSRMRHATF-----SAAWSLPG-----LGQD 411
 Db 352 -----QACSWADSLGPPKFDMLLMKMTGLNNTSVCALEPSCGCTPLPSMASTRALGEE 406
 QY 412 TLVP-PVYTVSQWRSD-VQFAKMHLLCPDVSYRHG--LLIALLALLTLTLCGWLALTC 467
 Db 407 LLQDFRSHQCMQWLNDDNMGSW---ACPMCKYIHRRWLVWVLAACLLAAALFFLLKK 463

QY 468 RRQSGPGPARPVLLLHAADSEAOQRLVGALELLRAALGGGRDVIIVDLWEGRHRVARVP 527
 Db 464 DRKAARG-SRTALLLHSDAGYERLVGALASLSOM---PLRVAVDLWSRRLSAHGA 519
 QY 528 LPWLWAARTVAREQGTVLLWSGA-----DLRPVS-GDPRAAPLLA-----LLH 572
 Db 520 LAWFHHQRRRILQGGVVILLFSPAAVAQCOOWLQLOQVTEPGPHDALAAMLSVLPDFLQ 579
 QY 573 AAPRPLLLLAYFRLCAKGDIPPLRALPRYRLRLDPLRLRALDARPAFAEATSWGLGA 632
 Db 580 GRATGRYGVYFDGLLHPDSVSPFRVAPLSLTQLPFAFLDALOG---GCSTSGRPAAD 636
 QY 633 RQRR-----QSRLELCS 644
 Db 637 RVERVTOALRSALDSCT 653

RESULT 8

US-09-899-471-8
 ; Sequence 8, Application US/09899471
 ; Patent No. US20020146763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gao, Zeren
 ; TITLE OF INVENTION: Murine Cytokine Receptor
 ; FILE REFERENCE: 00-46
 ; CURRENT APPLICATION NUMBER: US/09/899,471
 ; CURRENT FILING DATE: 2001-07-05
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 692
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-899-471-8

Query Match 8.7%; Score 304.5; DB 10; Length 692;
 Best Local Similarity 25.4%; Pred. No. 3.6e-17;
 Matches 176; Conservative 69; Mismatches 246; Indels 203; Gaps 36;
 QY 36 TRCPLASHTVELPISLAAPGPPSSPSQL---GVCESGTVPAVCASICCCQVAQVFNAGASS 91
 Db 78 TDCDLCLR---VAVHLAVHGWEEPEDEKFGGAADSGVEEPNALSQAQVVSFQ-AYP 133
 QY 92 TSWC-----RNPKSL-PHSSSIGDTRCQHLRGSCCLVVTCLRRRAITFPSPQTSPTPRDF 145
 Db 134 TARCVLLEVQVPAALVQFGQSVGS-----VVYDCFEAAL-----GSEVRW 174
 QY 146 ALKGNLRLIQ-RHGKVPF-----DWTGKMEVGT-----GYNRRWVQLSGGPEFS 189
 Db 175 SYTQPRYEKELNHTQOLPALPWLNVNSADGNVHLVNLVNSEQHFGLSLYWNQVGGPPK-- 232
 QY 190 FDLLEPEARAIRVTISSGPEVSRYRLCHOWALECEELSPYDVQKIVSGGHTVELPYEFLLP 249
 Db 233 -----PRW-----HKNLGTGPQIITLHNTDLVP 254
 QY 250 CLCIEASYLQEDTVRRKCKPQFQSWPBAYGDFWKSVFHTDYSOHTOMVVALTLR----- 303
 Db 255 CLCICQWVPLEPDSVRTNICPFREDPRAH--QNLWQAAR-----LRLTLQSWLLDA 303
 QY 304 -CPKLEALCORHWHITLCKDL-----PNATARESDGWVLEKVDL--HPOLCFKVOP 354
 Db 304 PCSLPAEALCWRAPGGDCQPLVPLSWENVTVDK-----VLEPPLKHPNLCVQV-- 356
 QY 355 WFSFGNSSH---VBC---PHQTGSLTSNNVMDTQAQOLILHFSRMRHATF--SAAWSL 406
 Db 357 -----NSSEKLOLQCEWLADSLGPLKDDVLLLETRGPQ-----DNRSLEPSCSCTSLP 406
 QY 407 G-----LGQDTLVPVYTVS-----QVWRSDVQFAKMHLLCPDVSYRH--LGLL 448
 Db 407 SKASTRAARLGE-----YLLQDLQSGCQLQWLWDDDLGALW---ACPMCKYIHRRWLV 456
 QY 449 IIALALLTLTLCGWVLAITCRREPQSGPGPARPVLLLHAADSEAOQRLVGALEL-----LR 503

Db	457	WLACLLFAAALSILLLK-KDHAKAARGAALLIYSADSGFERLVGALASALCOLPLR	515
QY	504	AALGGGRDVTDLWEGRHVARVCPPLWAAATRVAREOGTVLLWMSGADLR	555
Db	516	VA-----VDLWSRRELSAOGPVAFHAQRQTQLQEGGVVLLFSPGAVALCSEWLQD	567
QY	556	PVSGP---DPRAPLLALHAAAPRL-----LLLAYESRLCAKGDIPPLRLAPRYRL	605
Db	568	GVSGPGAHGPHDAFRASLSCVLPDFLQGRAPSGYVCACFDRLHLHPDAVPALFTVPVFTL	627
QY	606	LRDLPLRLALDARPPAEATSWGRLGARORROSR	639
Db	628	PSQLPDFLQALQ-QPRAPRS--QLQRAEAOVSR	658

RESULT 9

US-09-874-503-14
: Sequence 14, Application US/09874503
: Patent No. US20020177188A1
: GENERAL INFORMATION:
: APPLICANT: Chen, Jian
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Guney, Austin L.
: APPLICANT: Li, Hanzhong
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Hymowitz, Sarah G.
: APPLICANT: Tumas, Daniel
: APPLICANT: Starovasnik, Melissa A.
: APPLICANT: VanLookeren, Menno
: APPLICANT: Vandlen, Richard
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Yansura, Dantel
: TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
: FILE REFERENCE: P1381R1C1P3(US)
: CURRENT APPLICATION NUMBER: US/09/874, 503
: CURRENT FILING DATE: 2001-06-05
: PRIOR APPLICATION NUMBER: US 60/253,646
: PRIOR FILING DATE: 2000-11-28
: PRIOR APPLICATION NUMBER: US 60/244,072
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: US 60/242,837
: PRIOR FILING DATE: 2000-10-24
: PRIOR APPLICATION NUMBER: US 60/175,481
: PRIOR FILING DATE: 2000-01-11
: PRIOR APPLICATION NUMBER: US 60/191,007
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: US 60/213,807
: PRIOR FILING DATE: 2000-06-22
: PRIOR APPLICATION NUMBER: US 60/172,096
: PRIOR FILING DATE: 1999-12-23
: PRIOR APPLICATION NUMBER: US 60/138,387
: PRIOR FILING DATE: 1999-06-09
: PRIOR APPLICATION NUMBER: US 60/134,287
: PRIOR FILING DATE: 1999-05-14
: PRIOR APPLICATION NUMBER: US 60/131,022
: PRIOR FILING DATE: 1999-04-26
: PRIOR APPLICATION NUMBER: US 60/130,232
: PRIOR FILING DATE: 1999-04-21
: PRIOR APPLICATION NUMBER: US 60/113,621
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: US 60/085,579
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: US 09/854,208
: PRIOR FILING DATE: 2001-05-10
: PRIOR APPLICATION NUMBER: US 09/854,280
: PRIOR FILING DATE: 2001-05-20
: PRIOR APPLICATION NUMBER: US 09/816,744

Db 357 -----NSSEKQLQECWADSLGPKDDVLLLETRGPQ-----DNRSLCALPSPGCTSLP 406
QY 407 G-----LQDTLPVPVTVS-----QWRSDDVQFANKHLLCPDVSVERH-----444
Db 407 SKASTRAARLGE-----YLLQDLSQGCLQLWDDDLGALW---ACPMDKYIHKRWALV 456
QY 445 --LGLLLALLLTLTGV-----VLALTCRRPQSGPGP--ARVLLHHAADSEAQRRLVG 496
Db 457 WLACLLFAAALSLLLLKDKHANGWLRLKQDVRSGAARGRAALLLYSADDSGFFERLNG 516
QY 497 ALABEL-----LRAALGGRRDVIYDLWEGRHVARVGPLWMLWAARTKVARREQGTVLLWLSG 551
Db 517 ALASALCOLPRVA-----VDLWSRRELSAQGPVAFHQAORRQTLQEGGVVLLFSP 568
QY 552 ADLR-----PVSGP---DPPRAAPLLALLHAAPRL-----LLLAVFSLCAKGD 593
Db 569 GAVALCSEWQDGVSGFANGPHDAFRASLVCVLPDLOGRAGPSYVGACFDRLHLPDAV 628
QY 594 PPPLRALPRYRLRLDLPRLRLALDARPFABEATSWGRLGARQRQR 639
Db 629 PALFRTVPVTLPSQLPDFLQALQ-QPRAPRS--GRLOERAEQVSR 671

RESULT 10

US-10-000-157-14
; Sequence 14, Application US/10000157
; Publication No. US20020192673A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul L.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovasinik, Melissa.
; APPLICANT: Vanlookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P4(US)
; CURRENT APPLICATION NUMBER: US/10/000,157
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/172096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/175481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/213807
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/242837
; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: 60/244072
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/253646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/908827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/931836
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 14
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-000-157-14

Query Match 8.5%; Score 299; DB 9; Length 705;
Best Local Similarity 25.5%; Pred. No. 1.1e-16;


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RESULT 12
US-09-816-744-14
, Sequence 14, Application US/09816744
, Publication No. US20030003546A1
, GENERAL INFORMATION:
, APPLICANT: Chen, Jian
, APPLICANT: Filaroff, Ellen
, APPLICANT: Fong, Sherman
, APPLICANT: Goddard, Audrey
, APPLICANT: Godowski, Paul
, APPLICANT: Grimaldi, Christopher
, APPLICANT: Gurney, Austin
, APPLICANT: Li, Hanzhong
, APPLICANT: Hillan, Kenneth
, APPLICANT: Tumas, Daniel

```

```
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; FILE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P2(US)
; CURRENT FILING DATE: 2001-03-22
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 14
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-816-744-14

Query Match      8.5%; Score 299; DB 9; Length 705;
Best Local Similarity 25.5%; Pred. No. 1.le-16;
Matches 180; Conservative 69; Mismatches 243; Indels 214; Gaps 37;

QY 36 TRCPFLASHTEVLPISLAAPGGSPSSQSL-----GVCESTVPVAVCASICCOVAQVFNAGSS 91
DB 78 TDCDLCRLR---VAVHLAVHGHWEPEDEEKEFGGAADSVVEEPRNASLQAQVVLSEFQ-AYP 133
QY 92 TSWC-----RNPKSL-PHSSSIGDTRCOHLLRGSCCLVVTCLRRATITPPSPQTSPTDRDF 145
DB 134 TARCVLLEQVPAALVFOGSGVS-----VVYDCFEAL-----GSEVRIW 174
QY 146 ALKGPMLRTO-RHGKVFP-----DWTGKMEVGT-----GYNRKWLVSGLGPPS 189
DB 175 SYTPRYEKELNHTQQLPALPWLNVNSADGDNVHLVNLVSEEHGFLSLYWNVOVGPPK-- 232
QY 190 FDLPPARAIIVTISGPEVSRLCHQWALECEELSPDVOKIVSGGHTVELPYEFLLP 249
DB 233 -----PRW-----HKNITGPOIITLNTHTDLVP 254
QY 250 CLCIEASYLQEDTVRRKKCPFGSWPAGYSGDFWKSVEHFTDYSQHTQMVNMLTIR----- 303
DB 255 CLCQVWPLEPDSVTRNICFPREDPRAH-QNLWQAAR-----LRLTLQSWLLDA 303
QY 304 -CPLEALCQRHWHITCKOL-----PNATARESDGWYVLEKVDL--HPQLCFKVP 354
DB 304 PCSLPAAALCWAPGGDCQPLVPLPSWENVTDK-----VLEFPLKGHENLCVQV-- 356
QY 355 WFEFGNSH---VEC--PHOTGSLTSWNVSMDOAQQLILHFFSRMHATF--SAAWSLP 406
DB 357 -----NSSEKLQLOECLWADSLGPKDDVILLLETRGPQ-----DNRSICALPEPGCTSLP 406
QY 407 G-----LGQDTLPVPYTVS-----QVWRSDVQFAFKHLCLCPDVSYRH----- 444
DB 407 SKASTRAARLGE-----YLLQDLQSGQCLQLWDDDLGALW---ACPMDKYIHKRWALV 456
QY 445 --LGLLILALLLTLGV-----VLALTCRRPQSGPG-ARPVLLHHAADSEAQRRLVG 496
DB 457 WLACLLFAAALSILLKDKHAGKWLRLKQDVRSGAAAGRAALLLYSADDSGFERLVG 516
QY 497 ALAEL-----LRAALGGGRDVIDLEGRHVARVGPLWLVWAARTVAREQGTVLLWSG 551
DB 517 ALASALCQLPLVA-----VDMRSRELSAQGPVAFHFQAQRQTLOEGGVVLLFSP 568
QY 552 ADLR-----PVSGP-----DPAAPLALLHAAPRL-----LLIAYFSRLCAKGD 593
DB 569 GAVALCSEMLQDVGSGAGHPDAPRASLSCLVPLDFLAGRPGSVYVACGFRLHHPDAV 628
QY 594 PPLRALPRVRLRLDLPRLRALDAPFAEATSWGLGARQORROS 639
DB 629 PALFRIVPFTLPSQLPDFLQALQ-QPRAPRS--GRLQABQSVSR 671

RESULT 13
US-09-747-259-14

; Sequence 14, Application US/09747259
; Publication No. US20030008815A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; FILE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 14
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-747-259-14

Query Match      8.5%; Score 299; DB 9; Length 705;
Best Local Similarity 25.5%; Pred. No. 1.le-16;
Matches 180; Conservative 69; Mismatches 243; Indels 214; Gaps 37;

QY 36 TRCPFLASHTEVLPISLAAPGGSPSSQSL-----GVCESTVPVAVCASICCOVAQVFNAGSS 91
DB 78 TDCDLCRLR---VAVHLAVHGHWEPEDEEKEFGGAADSVVEEPRNASLQAQVVLSEFQ-AYP 133
QY 92 TSWC-----RNPKSL-PHSSSIGDTRCOHLLRGSCCLVVTCLRRATITPPSPQTSPTDRDF 145
DB 134 TARCVLLEQVPAALVFOGSGVS-----VVYDCFEAL-----GSEVRIW 174
QY 146 ALKGPMLRTO-RHGKVFP-----DWTGKMEVGT-----GYNRKWLVSGLGPPS 189
DB 175 SYTPRYEKELNHTQQLPALPWLNVNSADGDNVHLVNLVSEEHGFLSLYWNVOVGPPK-- 232
QY 190 FDLPPARAIIVTISGPEVSRLCHQWALECEELSPDVOKIVSGGHTVELPYEFLLP 249
DB 233 -----PRW-----HKNITGPOIITLNTHTDLVP 254
QY 250 CLCIEASYLQEDTVRRKKCPFGSWPAGYSGDFWKSVEHFTDYSQHTQMVNMLTIR----- 303
DB 255 CLCQVWPLEPDSVTRNICFPREDPRAH-QNLWQAAR-----LRLTLQSWLLDA 303
QY 304 -CPLEALCQRHWHITCKOL-----PNATARESDGWYVLEKVDL--HPQLCFKVP 354
DB 304 PCSLPAAALCWAPGGDCQPLVPLPSWENVTDK-----VLEFPLKGHENLCVQV-- 356
QY 355 WFEFGNSH---VEC--PHOTGSLTSWNVSMDOAQQLILHFFSRMHATF--SAAWSLP 406
DB 357 -----NSSEKLQLOECLWADSLGPKDDVILLLETRGPQ-----DNRSICALPEPGCTSLP 406
QY 407 G-----LGQDTLPVPYTVS-----QVWRSDVQFAFKHLCLCPDVSYRH----- 444
DB 407 SKASTRAARLGE-----YLLQDLQSGQCLQLWDDDLGALW---ACPMDKYIHKRWALV 456
QY 445 --LGLLILALLLTLGV-----VLALTCRRPQSGPG-ARPVLLHHAADSEAQRRLVG 496
DB 457 WLACLLFAAALSILLKDKHAGKWLRLKQDVRSGAAAGRAALLLYSADDSGFERLVG 516
QY 497 ALAEL-----LRAALGGGRDVIDLEGRHVARVGPLWLVWAARTVAREQGTVLLWSG 551
DB 517 ALASALCQLPLVA-----VDMRSRELSAQGPVAFHFQAQRQTLOEGGVVLLFSP 568
QY 552 ADLR-----PVSGP-----DPAAPLALLHAAPRL-----LLIAYFSRLCAKGD 593
DB 569 GAVALCSEMLQDVGSGAGHPDAPRASLSCLVPLDFLAGRPGSVYVACGFRLHHPDAV 628
QY 594 PPLRALPRVRLRLDLPRLRALDAPFAEATSWGLGARQORROS 639
DB 629 PALFRIVPFTLPSQLPDFLQALQ-QPRAPRS--GRLQABQSVSR 671
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Db 134 TARCALLEVQVPAALVQFGSGVS-----VYDCEFAAL-----GSEVRW 174
 QY 146 ALKGNLRIO-RHGKVP-----DWTGKMEVGT-----GYNRRWVQLSGGPEFS 189
 Db 175 SYTOPRYEKLNHQQLPALPWLNVNSADGNVHLVNLVNSEQHFGLSLYNVQVQPPK-- 232
 QY 190 FDLLEPAAIRVTISSGPEVSVRLCHQWALECEELSSPYDVQKIVSGGHTVPELPEFLP 249
 Db 233 -----PRW-----HKNLTGPOIITLHNTDLP 254
 QY 250 CLCIEASYLOEDTVRRKKCFQSWPEAYGDFWKSVMHTDYSHQTMWMAITLR----- 303
 Db 255 CLCQVWPLEPDSVTRNICPEREDPRAH-QNLWQAAR-----LRLTLQSWLLDA 303
 QY 304 -CPLKLEAALCORHWTCLCKDL-----PNATARESDGWVYLEKVDL--HPQLCFKVP 354
 Db 304 PCSLPAEALCWAPGGDCQPLVPLSWENVTVDK-----VLEPPLKGHPNLCVQV-- 356
 QY 355 WFSFGNSH-----VEC--PHQTGSLTSMNVSMDTQAQQLILHFSRHMATF--SAAWSLP 406
 Db 357 -----NSSEKLQLECLWADSLGPKDDVLLLETRGPQ-----DNRSICALPEPGCTSLP 406
 QY 407 G-----LGQDTLVPVTVS-----QWRSDVQFAWKHLLCPDVSYRH----- 444
 Db 407 SKASTRAARLGE-----YLLQDLQSGQCQLQWDDDLGALW---ACPMKDYIHKRWALV 456
 QY 445 --LGLLILALLLTLLGV-----VLATCRRRPQSGPGP-ARPVLLLHAAADSEAOORLVG 496
 Db 457 WLACLLFAAALSLLLLKKHAKGWLRLKQDVRSGAARGRAALLLYSADDSGFERLVG 516
 QY 497 ALAEL-----LRAALGGGRDVIDLWEGRHVARVGPPLWMAARTVAREOGTVLLWSG 551
 Db 517 ALASALCQLPLRVA-----VDLWSRRELSAQGPVAFWFAHQRTQLEGGVVVLLFSP 568
 QY 552 ADLR-----PVSGP---DPRAAPLALLHAAAPRL-----LLLAYFSRLCAKADI 593
 Db 569 GAVALCSEWLQDVGSGPGAHGPHDAFRASLSCVLPDLQGRAPGSYVGCDFRLLHPDAV 628
 QY 594 PPLRALPRYLRLDRLPRLRLALDARPAEATSWGRLGARQRROR 639
 Db 629 PALFRTVPVFTLPQLPDLFGALQ-QPRAPRS--GRQERAEQVSR 671

RESULT 14

US-10-174-590-598
 ; Sequence 598, Application US/10174590
 ; Publication No. US20030008352A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C42
 ; CURRENT APPLICATION NUMBER: US/10/174,590
 ; CURRENT FILING DATE: 2002-06-18
 ; Prior application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 598
 ; LENGTH: 705
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien

Query Match

8.5%; Score 299; DB 9; Length 705;

Best Local Similarity 25.5%; Pred. No. 1.1e-16;
 Matches 180; Conservative 69; Mismatches 243; Indels 214; Gaps 37;

QY 36 TRCPPLASHTVLPISLAAPGGPSSQSL-----GVCESGTVPACASICCCQVAVENGASS 91
 Db 78 TDCDLCLR---VAVHLAVGHWEPEDEEKFGGAADSGVEEPRNASLQAOVVLFSQ-AYP 133
 QY 92 TSWC-----RNPKSL-PHSSSIGDTRCHLLRGSCCLVTRRAITFPSPQTSPTPRDF 145
 Db 134 TARCALLEVQVPAALVQFGSGVS-----VYDCEFAAL-----GSEVRW 174
 QY 146 ALKGNLRIO-RHGKVP-----DWTGKMEVGT-----GYNRRWVQLSGGPEFS 189
 Db 175 SYTOPRYEKLNHQQLPALPWLNVNSADGNVHLVNLVNSEQHFGLSLYNVQVQPPK-- 232
 QY 190 FDLLEPAAIRVTISSGPEVSVRLCHQWALECEELSSPYDVQKIVSGGHTVPELPEFLP 249
 Db 233 -----PRW-----HKNLTGPOIITLHNTDLP 254
 QY 250 CLCIEASYLOEDTVRRKKCFQSWPEAYGDFWKSVMHTDYSHQTMWMAITLR----- 303
 Db 255 CLCQVWPLEPDSVTRNICPEREDPRAH-QNLWQAAR-----LRLTLQSWLLDA 303
 QY 304 -CPLKLEAALCORHWTCLCKDL-----PNATARESDGWVYLEKVDL--HPQLCFKVP 354
 Db 304 PCSLPAEALCWAPGGDCQPLVPLSWENVTVDK-----VLEPPLKGHPNLCVQV-- 356
 QY 355 WFSFGNSH-----VEC--PHQTGSLTSMNVSMDTQAQQLILHFSRHMATF--SAAWSLP 406
 Db 357 -----NSSEKLQLECLWADSLGPKDDVLLLETRGPQ-----DNRSICALPEPGCTSLP 406
 QY 407 G-----LGQDTLVPVTVS-----QWRSDVQFAWKHLLCPDVSYRH----- 444
 Db 407 SKASTRAARLGE-----YLLQDLQSGQCQLQWDDDLGALW---ACPMKDYIHKRWALV 456
 QY 445 --LGLLILALLLTLLGV-----VLATCRRRPQSGPGP-ARPVLLLHAAADSEAOORLVG 496
 Db 457 WLACLLFAAALSLLLLKKHAKGWLRLKQDVRSGAARGRAALLLYSADDSGFERLVG 516
 QY 497 ALAEL-----LRAALGGGRDVIDLWEGRHVARVGPPLWMAARTVAREOGTVLLWSG 551
 Db 517 ALASALCQLPLRVA-----VDLWSRRELSAQGPVAFWFAHQRTQLEGGVVVLLFSP 568
 QY 552 ADLR-----PVSGP---DPRAAPLALLHAAAPRL-----LLLAYFSRLCAKADI 593
 Db 569 GAVALCSEWLQDVGSGPGAHGPHDAFRASLSCVLPDLQGRAPGSYVGCDFRLLHPDAV 628
 QY 594 PPLRALPRYLRLDRLPRLRLALDARPAEATSWGRLGARQRROR 639
 Db 629 PALFRTVPVFTLPQLPDLFGALQ-QPRAPRS--GRQERAEQVSR 671

RESULT 15

US-10-176-758-598

; Sequence 598, Application US/10176758
 ; Publication No. US20030008353A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C104
 ; CURRENT APPLICATION NUMBER: US/10/176,758
 ; CURRENT FILING DATE: 2002-06-21

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 28, 2003, 09:28:18 : Search time 22 Seconds
(without alignments)
2870.923 Million cell updates/sec

Title: US-09-863-818a-12
Perfect score: 3512
Sequence: 1 MGSSRLAALLPLLIIVIDL.....SRLELCRLREARLADLG 657

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	3.5	738	2 I49295	IL-12 receptor bet
2	114.5	3.3	635	2 A45866	MPL-P protein prec
3	113.5	3.2	923	2 A39596	progesterone recep
4	111.5	3.2	515	2 G75267	ABC transporter, p
5	110.5	3.1	381	2 S48049	cholecystokinin B
6	107.5	3.1	452	2 A46195	cholecystokinin B
7	105.5	3.0	923	2 T53280	progesterone recep
8	105.5	3.0	7576	2 T17428	FK506 polyketide s
9	105	3.0	523	2 A83106	hypothetical prote
10	104	3.0	709	2 F75584	hypothetical prote
11	104	3.0	732	1 JU0132	acylaminoacyl-pept
12	103.5	2.9	401	2 T36882	hypothetical prote
13	102.5	2.9	1034	2 JC5598	mucin - rat
14	102	2.9	579	2 B45366	MPL-K protein prec
15	102	2.9	829	2 B96840	hypothetical prote
16	102	2.9	930	2 A25923	progesterone recep
17	102	2.9	2035	2 AC0333	versiniaabactin bio
18	102	2.9	2041	2 T17439	peptide synthetase
19	101	2.9	428	2 S70670	3-deoxy-D-manno-2-
20	101	2.9	482	2 G83490	probable outer mem
21	101	2.9	906	2 G83156	probable transcrip
22	100.5	2.9	392	2 T46418	hypothetical prote
23	100.5	2.9	1438	2 T17402	dihydroaeruginoinc
24	100	2.8	1193	2 T50729	magnesium-protopor
25	99	2.8	404	2 T35421	probable regulator
26	99	2.8	560	2 T36054	probable two-compo
27	98.5	2.8	736	2 F70815	hypothetical prote
28	98	2.8	732	1 S07624	acylaminoacyl-pept
29	97.5	2.8	452	2 JC2459	gastrin/cholecysto

30 97 2.8 440 2 S77194 hypothetical prote
31 96.5 2.7 351 2 E75631 iron ABC transport
32 96.5 2.7 582 2 B45878 hypothetical prote
33 96.5 2.7 668 2 T01685 crpl protein - mai
34 96.5 2.7 3413 2 T17467 rifamycin polyketi
35 96 2.7 805 2 G87662 peptidase, M20/M25
36 95.5 2.7 559 2 F83283 precorrin-3 methyl
37 95.5 2.7 685 2 AC0527 ferrichrome transp
38 95.5 2.7 1407 2 T28702 probable polyketid
39 95.5 2.7 2205 1 MNWVRN nonstructural poly
40 95 2.7 396 2 S54999 ubiquinol-cytochro
41 95 2.7 453 2 S32817 gastrin receptor -
42 95 2.7 693 2 T25678 hypothetical prote
43 95 2.7 892 2 T29420 probable transcrip
44 95 2.7 1193 2 F83264 hypothetical prote
45 95 2.7 5149 2 F83345 probable non-ribos

ALIGNMENTS

RESULT 1
I49295
IL-12 receptor beta component precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49295
R:Chua, A.O.; Chizzonite, R.; Desai, B.B.; Truitt, T.P.; Nunes, P.; Minetti, L.J.; Wa
J. Immunol. 153, 128-136, 1994
A:Title: Expression cloning of a human IL-12 receptor component. A new member of the
A:Reference number: I37892; MUID:94267217; PMID:7911493
A:Accession: I49295
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-738 <RES>
A:Cross-references: EMBL:U03922; NID:g1046233; PIDN:AAA87457.1; PID:g1046234

Query Match 3.5%; Score 122; DB 2; Length 738;
Best Local Similarity 20.3%; Pred. No. 0.3;
Matches 128; Conservative 61; Mismatches 183; Indels 260; Gaps 36;

QY 38 CPLASHTVLPI-----SLAAPGPPSSPQSLGVCSCGTVPAVCASICCOVAQVFNQASS 91
DB 218 CPSENMAQEIQRRLRLSSGAPGWSQMPVC-----VP----- 254
QY 92 TSWCRNPKSLPHSSIGDTRCQHLRLGSCCLVVTCLRRATIF--PSPQOTSPTDRFALKG 149
DB 255 -----PEVLPOAKI--KFLVEPLNOGG-----RRRLTMQGSFQLAVPE---GCRG 295
QY 150 -PNLRQIRHGKVF-----PDWTHGMEVGTGYNRRWVOLSGGPEFFSFDLLPEARAIRV 201
DB 296 RPAQVKKHLVLRMLSCRCQAQTSKTVPLGKKLN-----LSGA-TYDLNLVLAKTFRGSR 349
QY 202 TISSGPEVSVRLCHOWALECEELSPPYQKIVSGGHTVELPYEFLLP--CLCIEASYLIQ 259
DB 350 TI-----QKHLPAQELTETRALNVSV-GGNWTSQMOWAAQPGTTTCLE----- 392
QY 260 EDTVRRKKCFPGSWPEAYSGDFWKSVHFTDYSOHTQWVMALTRCPLKLEALCQRHDWH 319
DB 393 -----WQPW-----FQHRNHTH-----CTLVPEEEDPAKMVTHSKS 424
QY 320 TLCKDLPLNATARESDGWYV---LEKVDLHPQLCFKQVPWFSGNSS-----HVECPHQ 369
DB 425 S-----KPTLEQEECYRITVFASKNPKNMLWATVLSYYFGGNASRAGTRPHVSVRNG 478
QY 370 TGSULTS--NNVSMDTQAQOLILHFFSSRMHATFSAANSLPGLGODTLVPPVYTSQV---- 423
DB 479 TGDVSVSVETASOLSCTCPGLVTQYVVRCEAE--DGANE-----SEWLVPB--TKTQVTLDG 530
QY 424 WRSDVOF-----AMKHLICP-----DVSYRHLGLLILAL-----LALLTLIG 460
DB 531 LRSRVMYKVQVRADTARLFGANSH---PQRFSEFVQISRLSIIFASLGSFASVLLVGLSG 587

QY 461 VV-----LALTC----- 467
Db 588 YIGLNRAWHLCPLPTPGSTAVEFPSCQKQWQNCNPFEDFEVLYPRDALVEMPGD 647
QY 468 -----RRQSGGPPA-----RPVLLHAADEAQR-RLVGALAEILRAA----- 505
Db 648 RGDGTESQAAPEACALDTRRL-----ETQRQVQVQALSEARRLGLAREDCPRGDLA 699
QY 506 -----LGG-----GRDVTDLWEGRHVARVGP 527
Db 700 HVTLPALLGGVTQAGASVLDLWRTHKTAEPGP 731

RESULT 2
A45266
MPL-P protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C:Accession: A45266
R:Vigon, I.; Mornon, J.P.; Cocault, L.; Mitjavila, M.T.; Tambourin, P.; Gisselbrecht, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992
A:Title: Molecular cloning and characterization of MPL, the human homolog of the v-mpl oncogene
A:Reference number: A45266; MUID:92302297; PMID:1608974
A:Accession: A45266
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-635 <VIG>
A:Cross-references: GB:M90102; NID:g184260; PIDN:AAA69971.1; PID:g184261
C:Keywords: transmembrane protein

Query Match 3.3%; Score 114.5; DB 2; Length 635;
Best Local Similarity 19.4%; Pred. No. 0.94;
Matches 111; Conservative 52; Mismatches 129; Indels 281; Gaps 34;

QY 31 LPHWTR-CPLASHEV---LPI-----SLAAPGSPSPQSLG 64
Db 84 MPHFTGYCYQPPDQEEVRLFFPLHLWKNVFLNOTRQVLFVDSVGLPAPPSTIRKMG 143
QY 65 VCESGTVPVAVCASICQVAVFNGASSTSW-----CRNPKSLPHSS 106
Db 144 -----GSQP-----GELQISWEEPAPEISDFLRYELRYGPRDK-----NS 179
QY 107 IGTRCQHLLRSGCGLV-----TCLRAITF-PSPQTSPTRD---FALKGP 150
Db 180 TGPTVIQIATETCPALQRPHSASALDQSPCAQPTMPQDGPQKTSRSEASALTAEQG 239
QY 151 NLRIQRHGKVFDPDTHKMGVGTGYNRRWVQSGGPEFSDLLPEARAIRVTISGGPEVS 210
Db 240 SCLI-----SGLPQNSY---WLQLRSEPD-----GISLGGSWG 270
QY 211 VRLCHQWALECEELSPYDVQKIVSGGHTVELPYE-----FLLPCLCIEASYLQEDT 262
Db 271 -----SWSLPV-----TVDLPGDAVALGLQCFTLDLKNVTCWQQQD 308
QY 263 V-----RRKKCPFGSP----- 274
Db 309 ASSQGFYHSRARCPRDRYPINWECBEEKTNPGLOTQPFQSRCHFKSRNDSIHLVEV 368
QY 275 -----EAY-GSDEW-----KSHFTDYQSHTQWVMAVTLRCLKLEAALCQRHD 317
Db 369 TPAGTVHSILGSPFIHQAVRLPPTNHLWREISSG-----HLEWQHPS 415
QY 318 W---HTLCKDLPNATARESOGWVYLE-----KVDLHPQLCFKVQ-----PW 355
Db 416 WAAQETCYQL-RYTGEGHGDWVLEPPLGARGGTLELRPSRYRLQRLARLNGPTYQGPW 474
QY 356 FSEGNSSHVCEPHQTSGLTSWNVSMDTQAOQLIL-----HFSRMRHAT 398
Db 475 SWSDDPRVE-----TATETAW-ISLVT-ALHLVLGLSAVLGLLLLRWQFPAYHRLRH-- 526

QY 399 FSAAW-SLPG-----LQO-----DT--LVPPVYTVS 421
Db 527 --ALWPSLDLHRLVGLQYLRDRTAALSPPKATVS 557

RESULT 3

A39596
progesterone receptor B form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 20-Aug-1999
C:Accession: A39596; I49111
R:Schott, D.R.; Shyamala, G.; Schneider, W.; Parry, G.
Biochemistry 30, 7014-7020, 1991
A:Title: Molecular cloning, sequence analyses, and expression of complementary DNA en
A:Reference number: A39596; MUID:91299759; PMID:2069958
A:Accession: A39596
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-923 <SCH>
A:Cross-references: GB:M68915; GB:J05333; NID:g200471; PIDN:AAA39971.1; PID:g200472
R:Hagihara, K.; Wu-Peng, X.S.; Funabashi, T.; Kato, J.; Pfaff, D.W.
Biochem. Biophys. Res. Commun. 205, 1093-1101, 1994
A:Title: Nucleic acid sequence and DNase hypersensitive sites of the 5' region of the
A:Reference number: I49111; MUID:95100931; PMID:7802637
A:Accession: I49111
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9 <HAG>
A:Cross-references: EMBL:U12644; NID:g639916; PIDN:AAA66067.1; PID:g639917
C:Superfamily: progesterone receptor; erba transforming protein homology
C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation;
F:555-819/Domain: erba transforming protein homology <ERBA>
F:557-577/Region: zinc finger
F:593-617/Region: zinc finger

QY 23 SAGIGFRLPHWTRCPPLASHTEVLPLIS-----LAAPGGSPSPQSLGVCESGTVFAPVACASI 78
Db 404 SAGASSSTTFDF-----PLAPAQAPSSRPEGAAGVAGGSPASSSG-----SAL 453
QY 79 CCOVAQVFNAGSSTSWCRNPKSLPHSSIGDTRCQHLLRSGCGLVVTCLRRATTFPSPPQ 138
Db 454 ECILYKA-----EAPTOGSFAPLPCKPPAAASCLLPRDSL-----PAAPG 494
QY 139 TSPT-----RDFALKG-PNLRIQRH-----GKVPDWHKMGVGTGYNRRWVQSLGGPE 187
Db 495 TAAAPAIYQPLGLNGLPQLGYQAALVLDLQVPPYPLN-----YLRPDSEASQSQ 546
QY 188 FSDLLPEARAIRVTISSGPEVSVRLCHQWALECEELSPYDVQKIVSGGHTVELPYEFL 247
Db 547 YGFDLSLPQ-----KICLICGDEAG--CHYGVLTG--SKVFFKAMEGOHNY----- 591
QY 248 LPLCLCIEASYLQEDTVRRKKCP-----FQSWPEAYGSDFWKSVHFTDYS-QHTQWMA 299
Db 592 ---LCAGRNDCIVDKIRKKNCPACRLKCKCQAGVGLGGRKFK--FNKVRVVRTLDGVA 645
QY 300 LTRCLPCLKEA-ALCQRHDWHTLCKDLPNATARESOGWVLEKVDLHP---QLCFKVQPW 355
Db 646 LPQSVGLPNESQALSQRITFS-----PN-----QEIQLVPPPLINLLMSIEPD 687
QY 356 FSPGNSSHVCEPHQTSGLTSWNVSMDTQAOQLILHFSRMRHATFSAW--SLPGLGQDTL 413
Db 688 VIYAGHONTKPDTSSTLSLTSLNGERQLLSVV-----KWSKSLGFRNLHI 734
QY 414 VPPVYTVSQWRSVDQF--AWKHLLCPDVSYRHL 445
Db 735 DDQITLIQYSWMSLMVFLGWR-----SYKHV 761

RESULT 4

G75267
ABC transporter, permease protein, CystW family - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans

10

Db 5420 A-----ERYGLHPALLGAALALAGEG-----ADLPSAFDVRVHATGATTVRVAVTA 5466
Qy 376 WNVSMQTQAQQLLHFSSRHATFSAAMSLPGLGODTL-----VPPVTVSQVMSDVOF 430
Db 5467 TGHLEADETGSPVATGVARRRPLVEGAVPGLLRPDIAEIAELPPT-TATTTGGLDLP-- 5523
Qy 431 ANKHLCPDV-----SYRHGLGLLILALL-ALLT---LLGVVLTALTCRRPQS 472
Db 5524 -----VVPDWWILPAHGTGGGLGETRDLGARVLAAALRSFLTDDRYADAVLAV-----HT 5573
Qy 473 GPG--PARPVLLHAADSQAORRLVCAAE-----LLRAALGGGRDIVDLWEGRHVAR 524
Db 5574 GFLAPAAAGLVRTAQAEHPRIIVVDPAEPPTAAPLAAAGLGEPOQV-LREGRAYAR 5632
Qy 525 -----VGPELWMAARTVRAREOQTVLLWSGADLRPVGPDPRAPLPLA---LLHAA 574
Db 5633 RLTPAVPSGDAPEL-----DPDGTVL-----ITGSGTLAGIVARHLVGHG 5674
Qy 575 PRPLLILAYFSLCAKGDIP 594
Db 5675 VRRLLML-----SRGGTASDVP 5691

RESULT 9

A: Molecule type: DNA

A: Residues: 1-523 <STO>

A: Cross-references: GB:AE004848; GB:AE004091; NID:99950537; PIDN:AAG07708.1; GSPDB:GN001

A: Experimental source: strain PA01

A: Gene: PA4320

Query Match 3.0%; Score 105; DB 2; Length 523;
Best Local Similarity 22.2%; Pred. No. 3.9;
Matches 105; Conservative 44; Mismatches 143; Indels 182; Gaps 25;

Qy 301 TLRCPLK-----LEAALCORHDWHTLCKDLP-----NATARESD 334
Db 88 TLQALRAYPALLRKQLPASLLWRFSPTRSFDLPVLOGLAGEPRSORLIVLSQRNAG 147
Qy 335 GWVLEKVDLHPOLCFKVPWFSGNSHVCPHQTSLSWNVSMDFQAQQLIL--HFS 392
Db 148 GATWLTVVGVHLEMAL-----WAGFAMILYLLIPANEIDWNQSLDPEAGEWLEHLS 203
Qy 393 SRMHATFSAANSLPGLGODTLVPPVY-----TVSQVWRSVQFAWKHLCPDV 440
Db 204 NLLYVLVWVE-----PIYVACGFTLYLNRRTLEAW--DIELVFRRL----- 245
Qy 441 SYRHGL-----LLILALLALLTLGVVLTALTCRRPGCP-----ARPVLLLHAADSEARRL 494
Db 246 RQRLVGSAYVLLGLTASLAWL-----PAPSAYABPA-----AATSAGEAEL 287
Qy 495 VGALAEALLRAALG---GGRDV--IVD----- 515
Db 288 PPEQARLLRQKLSQAGKQIRAIVDGAPFNKSETVTVGWRFQDKTEKSKSKEDEERLKA 347
Qy 516 LWEG-----RHVARV--GPLPW-----LWAAR-----TRVAREOQT 544
Db 348 FFEALANVPRFRAHQVIEVLLWALLFSAVFLVVRVREWLRLFVGNLGLPORAREAPT 407

Qy 545 VLLWSGADLRPVSGPDPRAPLALLHAAPRPLLLAY---PSRLC-----AK 590
Db 408 VME---GDLSPESLPDDIASNAERLWNEKPREALGLLYRGLLSRLLDYRLPLKGSHT 464
Qy 591 GDIPPPRALPRYRLRLDLPRLLRALDARPAEATSWG-RLGARQRQRSLC 643
Db 465 GEVLREGLRQORPLHYSQLTAQ-----WQALAYGHRLPADDTTRQ---RLC 510

RESULT 10

F75584

A: Molecule type: DNA

A: Residues: 1-709 <WHI>

A: Cross-references: GB:AE001863; GB:AE001825; NID:G6460670; PIDN:AAF12514.1; PID:G646

A: Experimental source: strain R1

A: Gene: DR0305

A: Map position: 2

Query Match 3.0%; Score 104; DB 2; Length 709;
Best Local Similarity 26.2%; Pred. No. 6.6;
Matches 86; Conservative 23; Mismatches 105; Indels 114; Gaps 15;

Qy 398 TFSANSL---PGLGQDTLPPVTVTSQV-----WRS---DVQFAWKHLCP 438
Db 297 SLTALWGLDLPSPGEGFWTPLLRLVSPALVGLAGALRAAQWRARHPHTPLPWLACG 356
Qy 439 DVSRYHGLLLALLALLTL-LGVVLTALTCRRPQS GPG-----PARPVLL- 483
Db 357 AVLVLGDTGDTLLTLLTLLSALGVLAHRSALAPDLRGTLYWGCALPGLLGGFLIAR 416
Qy 484 -----HAADSEARQLRVGALAEALLRAAL-----GGRDIVDLWEGRHVARVGPPLW 532
Db 417 AVGGGAH-----SRLLVGSILAAALTALLTARQAQGGREKLGOAKLGQRTAEAGLVLLA 472
Qy 533 AARTVAREOQTVLLWSGADLRPVSGPDPRAPLALLHAAPRPLLLAYFSLCAKGD 592
Db 473 LALTFMAR-----PAQFAPALAL-----TALVAALLPLRVGE 505
Qy 593 IPPPLRALPRYRLRLDLPRLL-----RALDARPAEATSW-----G 628
Db 506 -----RVWLLLLGLPALAKWQWLASSALWQEEANAQPLALLGALLLVSWLTQDDTG 558
Qy 629 R--LGARQRQRSLCRLEREAAALA 654
Db 559 RWLSARVPARSALVL-----RRLPRLA 581

RESULT 11

JU0132

A: Molecule type: mRNA

N: acylaminoacyl-peptidase (EC 3.4.19.1) [validated] - pig

C: Species: Sus scrofa domestica (domestic pig)

C: Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jul-2000

C: Accession: JU0132

R: Mitsu, M.; Asada, K.; Uchimura, Y.; Kimizuka, F.; Kato, I.; Sakiyama, F.; Tsunawasa

J. Biochem. 106, 548-551, 1989

A: Title: The primary structure of porcine liver acylamino acid-releasing enzyme deduc

A: Reference number: JU0132; MUID:90110044; PMID:2691504

A: Accession: JU0132

A: Molecule type: mRNA

A:Residues: 1-732 <MIT>

C:Genetics:

A:Introns: 4/3; 49/1; 91/2; 122/3; 148/1; 202/3; 248/3; 279/2; 293/1; 333/3; 354/1; 386/

C:Function:

A:Description: EC 3.4.19.1 [validated, MUID:90110044]

C:Superfamily: acylaminoacyl-peptidase

C:Keywords: acetylated amino end; homotetramer; hydrolase; omega peptidase

F:1/Modified site: acetylated amino end (Met) #status experimental

F:587,675,707/Active site: Ser, Asp, His #status predicted

Query Match 3.0%; Score 104; DB 1; Length 732;

Best Local Similarity 21.2%; Pred. No. 6.9;

Matches 78; Conservative 45; Mismatches 141; Indels 104; Gaps 18;

QY 136 PPTSTPTDFALKGNLRIQRHGVFDPWTHKGEVGTGY--NRR-----VWQLSGGPEFS 189

DB 241 PESVSPGQAFWAPGDT-----GVVFGVWHEPFLRGIRFCNRRSALYYVDLTGG---K 291

QY 190 FDLLEPRAIRITISSGPEVSRLC-----HWALECEELSSPYD---VQKI 233

DB 292 CELLSQ-ESVAVT---SPRLSPDQCRIVYLFPSLVPHQ---QCQLCL-YDWYTRVTSV 343

QY 234 V-----SGHVTVELPYEFLPCLCIEASYLQEDIVRRKKKCPFGSWPAYGS-- 279

DB 344 VVDIVPRQLGEDFSGIYCSLLP---LGCWSGADSQRVFDSPQRSQDLFAVDQMGSVT 399

QY 280 -----DFKWSVHTFDYSQHTQMWALTLRCLKLEAALCQRHDWHTLCKDLPNATAR 331

DB 400 SITAGSGGSMK---LLTIDRLMVQFSTFSPVPSLVKGF-----LPPAGKE 444

QY 332 ESDGVMVLEKVDLPQLCFKQVPWFSGNSSHVE---CPHOTGSITSWNVSMDTQAQOLI 388

DB 445 QAVSVVLEAEAPFPDIDSWIRVLQPPQOEHVQYAGLDFEAILLQPSNPEKTQVPMV 504

QY 389 LHFSSRMHATSAANSL-----PGLQDQLVPPVYTVSVQWRSVDV 428

DB 505 MPHGQ-PPHSFVTAWMLFPAMLCMKGFALLVNVYRGSTGFGQDLSLPGNVGHQDKVDV 563

QY 429 OFAKHLL 436

DB 564 QFAVEQVL 571

RESULT 12

T36882

hypothetical protein SC151.19c - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000

C:Accession: T36882

R:Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1999

A:Reference number: 221617

A:Accession: T36882

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-401 <MUR>

A:Cross-references: EMBL:AL109848; PIDN:CAB52843.1; GSPDB:GN00070; SCOEDB:SC151.19c

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SC151.19c

C:Superfamily: probable hexosyltransferase ytxN

Query Match

Best Local Similarity 2.9%; Score 103.5; DB 2; Length 401;

Matches 91; Conservative 40; Mismatches 126; Indels 79; Gaps 19;

QY 356 FSGNSSHVECPHOTGSLTSWNVSMDTQAQQLLHFFSSRMHATFSAANSLPGLQDQLV 415

DB 79 FTGAGADHVHVRSSDPVSV--AALRTVCAEADLVHAHGLHASFRAALALG--GRVRTP 134

QY 416 PYTVTSQVW--RSDVQFAWKHLCLCPDVSRYRHLGLLILALLTLGLVVALT----- 466

DB 135 LVVVT-----WHDRAHAGARGQLL--RVLERRV-----MKAATVVVLGATSELVDGARRTG 182

QY 467 CRRPQSGPG--PARPVLLHHAADSEARRLV-----GALAELLRAALGG-----GRDVIVD 515

DB 183 ARDARLGPVALPARPGPPAGSDDDPDLRKPVAELGAIDRPLLVAVGSLRHRGYDVLDD 242

QY 516 ---LWEGRHVARVGPPLPWMAA-----RFRVAREOGTVLLWMSGADLRPVSGPDRP 563

DB 243 AARVWR-----RLDPAPLVVAVAGEPLRGELOGRIEGELPVVLVGSRDDV-----PDLL 292

QY 564 AAPLLALLHAAPRP-----LLLAYFSRL-----CAKGDIPPLRALPRYLLRLDPLRLRA 615

DB 293 AAADLALLLSRRRPGRSVLAQEAHALHARVPLVAGAVGIP-----ELVGDAELVPP 343

QY 616 LDARPAEATSWRGLGARQRQRSLRLECSRLEREAA 651

DB 344 GDAALADAVV--RLADPADQD--ELRERGTFQAA 375

RESULT 13

JC5598

mucin - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 05-Nov-1999

C:Accession: JC5598

R:Inatomi, T.; Tisdale, A.S.; Zhan, Q.; Spurr-Michaud, S.; Gipson, I.K.

Biochem. Biophys. Res. Commun. 236, 789-797, 1997

A:Title: Cloning of rat Muc5AC mucin gene: Comparison of its structure and tissue dis

A:Reference number: JC5598; MUID:97396181; PMID:9245735

A:Accession: JC5598

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1034 <INA>

A:Cross-references: GB:U83139; NID:g2315984; PIDN:AAC53312.1; PID:g2315985

A:Note: translation not complete

C:Comment: This protein is a high molecular weight glycoprotein which is a major comp

ntestinal tract and reproductive tract.

C:Genetics:

A:Gene: Muc5A

C:Superfamily: von Willebrand factor type C repeat homology

F:45-149/Domain: cysteine-rich <CYS>

F:762-830/Domain: von Willebrand factor type C repeat homology <VWC>

Query Match 2.9%; Score 102.5; DB 2; Length 1034;
Best Local Similarity 19.1%; Pred. No. 13;
Matches 94; Conservative 43; Mismatches 168; Indels 187; Gaps 26;

QY 14 LLIVIDLSDSAGIGFRHLPHWTRCPPLASHTEVLPISLAAPGGSPSQ-----SL 63

DB 570 LEYASLCAAGGVCIPWRSHNTNTCPPTCPEN---QVTPCGPSNPHYCYRNDLISLSL 625

QY 64 GVCESGTVPAVCAASICCOVAQVFNQ-----ASSTSWCRNPKSLP-----HSSST- 107

DB 626 AIQAGPKSECC--FCPDDMTLFSNDSICVPCQWCLGPHGEVPEPGHTISINCCDCIC 683

QY 108 --GDTRCOHLL-----RSGCCLVVTCLRRATFPSP---PQISPTR 143

DB 684 KEGTLTQCEKLCPOPTCPEPGFVPVSTALEAGQCQSCFSCVCSNSSHCPPLHCPSSSL- 742

QY 144 DFALKGNLRLQRHGVFPDW---THKGMV-GTGVNRRVQLSGGPEFDFLLPEARAI 199

DB 743 -----IVTEBETCCPSONCCKGCDVNGTLY----- 770

QY 200 RVTISSGPEVSRLCHQ-----WALECE-ELSS---PYDVQKIVSGGHTVEL 242

DB 771 ---QPGDVSSSILCERCLCEVSSNAFSDVFNCEITELCNTCPKGFYQTTTGGH- 822

QY 243 PYELLPLCL--CTEASVLEQEDTVRRKKCPQSWPEATG-----SDFWKS-----VHFTDY 290

DB 823 -----CCGQCVP-----KTCPEKSNNSNLSLYKPGFEWPEPGNCPVTHKCEK 864

QY 291 SOHTQMWALTLRCLKLEAALCQRHDWHTLCKD-----LPNATARESDGNVLEKVD 343

DB 865 FQDVLTVTVTKIECP-KINCP---QDWAQLREDGCCYDCLVFQ-----QKCT 907

QY 344 LHP-QLCFKVPWFSGNSHVECPHOTGSLTSWN-----VSMDTQAQOLI 388
 Db 908 VHQROILRQNCSEGGPVSLSYCOGNGDSTSMYLEANVEHTCECQELQTSQSVT 967
 QY 389 LHFSSRMHATFS 400
 Db 968 LHCDDGSSRTFS 979

RESULT 14

B45266
 MPL-K protein precursor - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
 C:Accession: B45266
 R:Vigon, I.; Mornon, J.P.; Cocault, L.; Mitjavila, M.T.; Tambourin, P.; Gisselbrecht, S.
 Proc. Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992
 A:Title: Molecular cloning and characterization of MPL, the human homolog of the v-mpl c
 A:Reference number: A45266; MUID:92302297; PMID:1608974
 A:Accession: B45266
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-579 <VIG>
 A:Cross-references: GB:M90103; NID:g184262; PIDN:AAA69972.1; PID:g184263

Query Match 2.9%; Score 102; DB 2; Length 579;
 Best Local Similarity 18.1%; Pred. No. 7.4; Indels 251; Gaps 29;
 Matches 96; Conservative 53; Mismatches 131;

QY 31 LPHMNR-CPLASHTV-----LPI-----SLAAGGSPSSPSISG 64
 Db 84 MFHCTRYVCOFPDQEEVRLFFLHLWKVFNLTQTRQVLFVDSVGLPAPPSIIRAMG 143
 QY 65 VCESGTVPAVCASICCAQVAFNGASSTW-----CRNPKSLPHSS 106
 Db 144 ----GSQP-----GELQISWEEPAPEISDFLRYELRYGPRDPK-----NS 179
 QY 107 IGDTRCOHLRGSCCLVY-----TCLRRATF-PSPQTSPTRD-----FALKGP 150
 Db 180 TGPVLIQIATETCPALQPHSASALDQSCAQPTMWDQGPQKQTSFRESALTAEGG 239
 QY 151 NLRIQRHGVFPDTHKMGVEGTGYNRWVQLSGGPEFSFOLLPEAIRVITISSGPEVS 210
 Db 240 SCLI-----SLQPGNSY---WLQLRSEPD-----GISLGSGW 270
 QY 211 VRLCHQWALECEELSSPDVOKIVSGGHTVELPYE-----FLPLCLCTEASTLQEDT 262
 Db 271 ----SWSLPV-----TVDLPGDAVALGQCFTLDLKNVTCOMQOQDH 308
 QY 263 V-----RRKKCPQSWP----- 274
 Db 309 ASSQGFYHSRARCPRDYPPIWNECEETNPGLOTQPSRCHFKSRNDSIITHILEV 368
 QY 275 ----BAY-GSDPW-----KSVHFTDYSOHTQMVMALTLRCPKLKLEALCORHD 317
 Db 369 TTAGTGVHSYLGSPFWIHOAVRLPTPNLHREISSG-----HLELEWQHPS 415
 QY 318 W--HPLCKDLNPATARESDGHWVLE-----KVDLHPQLCFKQV-----PW 355
 Db 416 WAAQETCYQL-RYTGEGHQDKVLEPPLGARGGTLELRPRSRYLQRLARLNGPTYQGPW 474
 QY 356 FSGNSSHVECPHOTGSLTSNNVSMMDTQAQOLIILHFSSRMHATFSAAWSLP 406
 Db 475 SWSDPTRVE---TATETAW-ISLVT-ALHLVLGLSAVL-GLLLLRWQFP 518

RESULT 15

B96640
 hypothetical protein T25B24.15 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C:Accession: B96640

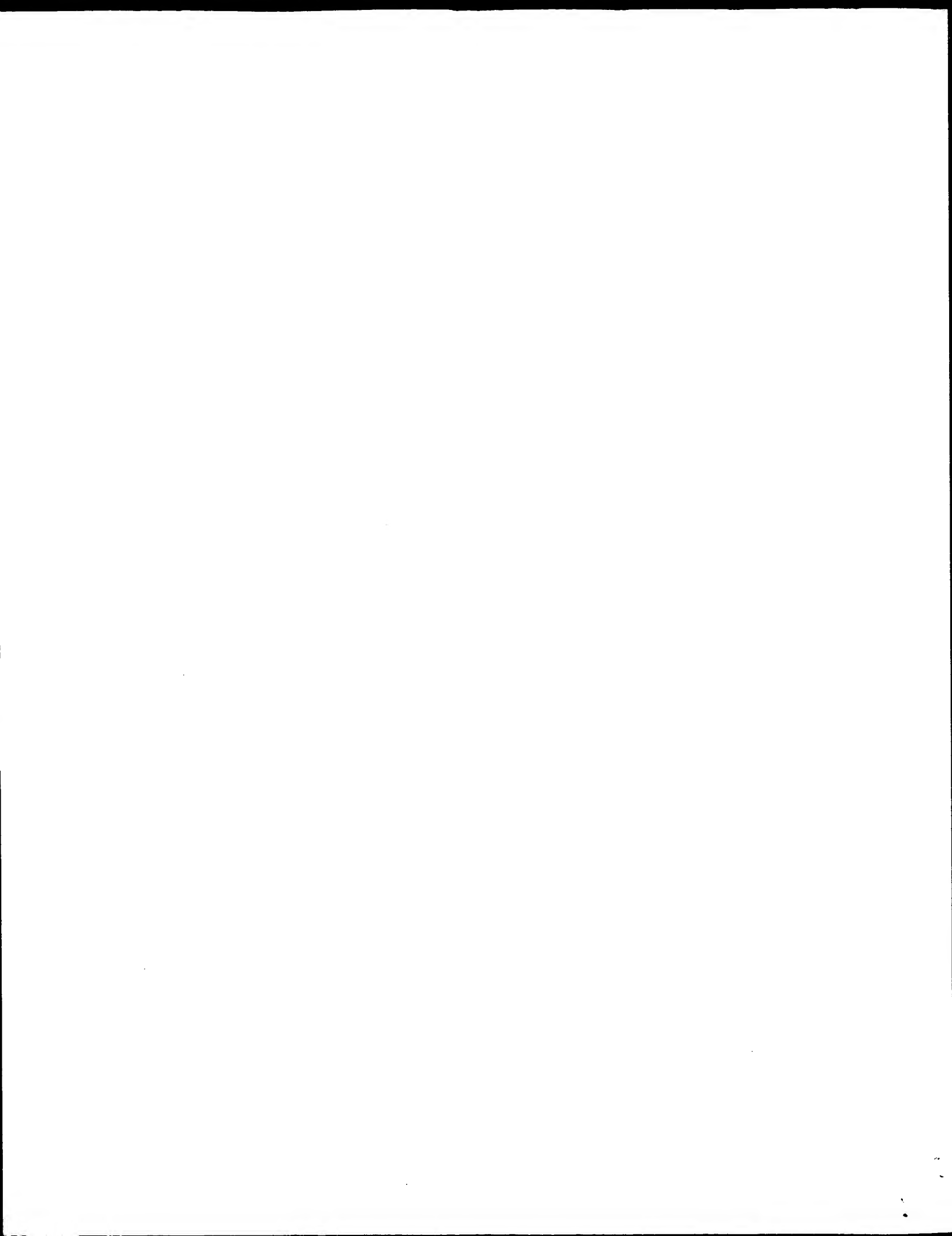
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96640
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-829 <STO>
 A:Cross-references: GB:AE005173; NID:g4585885; PIDN:AAD25558.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: T25B24.15
 A:Map position: 1
 C:Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprot

Query Match 2.9%; Score 102; DB 2; Length 829;
 Best Local Similarity 19.5%; Pred. No. 11;
 Matches 121; Conservative 64; Mismatches 165; Indels 270; Gaps 34;

QY 4 SRLAALLPLLLIVLDLSDSAGIGFRHLPHWNTRCP-----LASHTVELPLSLAAGGP 57
 Db 3 TRFACLLHFTMLFTLLSGSSAVI-----TTESPLSMGOTLSSANEVELGFFSPNN- 55
 QY 58 SSPQSLGVCESGTVPAVCASICCAQVQV-----FNGASSTSW----- 94
 Db 56 TQQYGVGIMFKDIPRVVWVANREXPVDTSTAYLAISSGSLLLNGKRGTVWSSGVF 115
 QY 95 ----CR-----NPKSLPHSS-----IGDTRCOHLRGSCCL--VVTCLRRAT 132
 Db 116 SSSGCRAEALSDSGNLKVIDNVSERALWQSPDHLGDT----LLTSSLTYNLATAERVL 171
 QY 133 F-----PSP-----PQTSPTROPALK-----GNLRIQRHGVFPDTHKG-- 168
 Db 172 SWSKYTDPSDFGLQITPQV-PSQGFVMRGSTPYWRSGPWAKTRFTGIPFMDSEYTGPF 230
 QY 169 ---MEV-GTG---YNRRWVQLSGGPEFSFOLLPEAIRVITISSGPEVSRLCHOWALEC 221
 Db 231 TLHQDVNGSGYLTYFQDYKLS-----RITLTS--EGSIKMF----- 266
 QY 222 EELSSPDVOKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPQSWPEAYGSDP 291
 Db 267 ----DNGMGWELYE-----APKLCDFYAGCGPFG--- 293
 QY 282 WKSVMHFTDYSOHTQMVMALTLRC-----PLKLEALCORHDW-----HTLCKDLNPA 328
 Db 294 ----LCVNSPSPMCKCFRGFVPKSVEE--MKRGNWTGGCVRHTELDCLGNS 338
 QY 329 TARESDGWVYLEKVDLHPQLCFKVPWFSEFNS-----SHVECPHOTGSLT----- 374
 Db 339 TGEDAD-----DFHQIANIKPPDFYEPASSVNAEECHQRCVHNCSCLAFAVKGIGC 390
 QY 375 -SNVSMDTQAQOLIILHFSSRMHATFSAAWSLPL-----GQDTLVPVPV----- 417
 Db 391 LVNQDLMDAVQ-----FSATGELLSIRLARSELDGNNRKRKTIVASIVSLTL 437
 QY 418 ----YTVSOVWRSDYQFANKHLCLCPDVSRYRHGLLILALLA--LLTLGVVLALTCRR- 469
 Db 438 FMILGTFAGVWRCRVE-----HIGNILMTLLSNDLLLFN---SFAKRR 480
 QY 470 ----PQSGPG 475
 Db 481 KAHISKDANKDLKPQDVP 500

Search completed: January 28, 2003, 09:30:58
 Job time : 32 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 28, 2003, 09:23:03 ; Search time 15 seconds
(without alignments)
1816.663 Million cell updates/sec

Title: US-09-863-818a-12

Perfect score: 3512

Sequence: 1 MGSSRLAALLPLLLIVIDL.....SRLELCSRLEREAARLADLG 657

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	126	3.6	866	117R_HUMAN	Q96f46 homo sapien
2	125.5	3.6	1115	1 TBC2_CHLRE	Q8vxp3 chlamydomon
3	122	3.5	738	112R_MOUSE	Q60837 mus musculus
4	121.5	3.5	864	117R_MOUSE	Q60943 mus musculus
5	114.5	3.3	635	1 TPOR_HUMAN	P40238 homo sapien
6	113.5	3.2	923	1 PRGR_MOUSE	Q00175 mus musculus
7	113.5	3.2	1199	1 Y173_HUMAN	Q14679 homo sapien
8	107.5	3.1	452	1 GASR_RAT	P30553 rattus norv
9	105.5	3.0	923	1 PRGR_RAT	Q63449 rattus norv
10	104	3.0	732	1 ACPH_PIG	P19205 sus scrofa
11	104	3.0	1202	1 JAG2_RAT	P97607 rattus norv
12	104	3.0	1247	1 JAG2_MOUSE	Q9qy65 mus musculus
13	102	2.9	930	1 PRGR_RABIT	P06186 oryctolagus
14	101.5	2.9	1088	1 PIGO_HUMAN	Q8teq8 homo sapien
15	100.5	2.9	685	1 FHUB_SALTY	O87656 salmonella
16	100	2.8	1193	1 BCBH_RHOSH	O9rfd5 rhodobacter
17	99.5	2.8	1093	1 PIGO_MOUSE	Q9jjj6 mus musculus
18	99.5	2.8	1435	1 Y194_HUMAN	Q12766 homo sapien
19	99	2.8	453	1 GASR_MOUSE	P56481 mus musculus
20	98	2.8	732	1 ACPH_RAT	P13676 rattus norv
21	97.5	2.8	316	1 UNG_PVKRA	P52507 pseudorabie
22	97.5	2.8	452	1 GASR_MOUSE	P46627 oryctolagus
23	96.5	2.7	948	1 CHRD_MOUSE	Q9z0e2 mus musculus
24	96.5	2.7	1964	1 NTCA_MOUSE	F31695 mus musculus
25	95.5	2.7	2205	1 POLN_RUBVT	P13889 rubella vir
26	95	2.7	396	1 CYB_PETNA	Q35534 petromyzon
27	95	2.7	453	1 GASR_CANFA	P30552 canis fami
28	94.5	2.7	955	1 CHRD_HUMAN	O9h2x0 homo sapien
29	94	2.7	657	1 DCTS_RHOCA	P37739 rhodobacter
30	93.5	2.7	761	1 PQOE_KLEPN	P27508 klebsiella
31	93.5	2.7	910	1 DDRI_RAT	Q63474 rattus norv
32	93.5	2.7	3718	1 LMA5_MOUSE	Q61001 mus musculus
33	93	2.6	573	1 AMH2_HUMAN	Q16671 homo sapien

34	93	2.6	1238	1 JAG2_HUMAN	Q9y219 homo sapien
35	92.5	2.6	491	1 A2AP_HUMAN	P08697 homo sapien
36	92.5	2.6	513	1 ENV_BLV82	P25506 bovine leuk
37	92.5	2.6	515	1 ENV_BLV85	P25507 bovine leuk
38	92.5	2.6	555	1 MIS_MOUSE	P27106 mus musculus
39	92.5	2.6	665	1 DUSX_HUMAN	Q9by84 homo sapien
40	92.5	2.6	795	1 DEGY_CAEEL	O01635 caenorhabdi
41	92.5	2.6	2144	1 CLR2_RAT	Q9qyp7 rattus norv
42	92	2.6	1246	1 SKIW_HUMAN	Q15477 homo sapien
43	92	2.6	2003	1 NTC4_HUMAN	Q99466 homo sapien
44	91.5	2.6	294	1 HUPK_RHOCA	P30797 rhodobacter
45	91.5	2.6	933	1 PRGR_HUMAN	P06401 homo sapien

ALIGNMENTS

RESULT 1

ID	117R_HUMAN	STANDARD;	PRT;	866 AA.
AC	Q96f46; O43844;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-17 receptor precursor (IL-17 receptor).			
GN	IL17R.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=T-cell;			
RX	MEDLINE=98035683; PubMed=9367539;			
RA	Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,			
RA	VandenBos T., Zappone J., Painter S.L., Armitage R.J.;			
RT	"Molecular characterization of the human interleukin (IL)-17			
RT	receptor.";			
RL	Cytokine 9:794-800(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Uterus;			
RL	Straussberg R.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,			
CC	suggesting that additional components are involved in IL17-induced			
CC	signaling.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).			
CC	-!- TISSUE SPECIFICITY: Widely expressed.			
CC	-!- PTM: Glycosylated.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U58917; AAB99730.1; --			
DR	EMBL; BC011624; AAH11624.1; --			
DR	Genew; HGNC:5985; IL17R.			
DR	MIM; 603461; --			
KW	Receptor; Transmembrane; Signal; Glycoprotein.			
FT	SIGNAL	1	31	POTENTIAL.
FT	CHAIN	32	866	INTERLEUKIN-17 RECEPTOR.
FT	DOMAIN	32	320	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	321	341	POTENTIAL.
FT	DOMAIN	342	866	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	810	818	POLY-GLU.
FT	CARBOHYD	49	49	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	54	54	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	206	206	N-LINKED (GLCNAC. . .) (POTENTIAL).

Db 575 GEVALSLNALGRL--SAVMDLPLALIDLMSGRVLDLTSRLIAAGFGSGELQLLEGLT 632
 QY 449 ILAL-----LALLTLGLWALATCRPSQPGPARPVLLILLHARDS 488
 Db 633 RLALQPLENMQAFVAALQPLDKLDAQGLVNSLAQ--QYRQPMQMEVVLIAATQA 690
 QY 489 E-----AQRL-----VGALAEALLRAALGGGRDVIDVLWEGRHVAR 524
 Db 691 NMKQLLADTCSAALLTALRLNLEIPPPGWGALLEERSAL---KNRCTDL---HLAN 743
 QY 525 V-GPL-PW-----LWAARTVAREQGVTVLLWSCADLRPVSGPPRAAPLALLHA--- 573
 Db 744 LAGSLAAGVPRDGRWAAR-----LMWRSQVLMNEDRMSRA--LVALIQAMVS 790
 QY 574 ---APRPLLLAYFSLCAK-----GDIPPLRAL-----PRYLLRLDLP 610
 Db 791 LGLSNPV-----WTQLCLQAAVRASQAPPEPHYGTMLASLHAGLQPPQEWLRLML 845
 QY 611 RLRLDALRPAEATSWGR-----LGARQRRQ--SRLELCSRLEREAAALAD 655
 Db 846 STYRCWDR---FSVTHWSSLLPALVLLKARPPREWLRFEATS-----AARLAD 891

RESULT 3
 IL12R_MOUSE
 ID IL12R_MOUSE STANDARD; PRT; 738 AA.
 AC Q60837;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-12 receptor beta-1 chain precursor (IL-12R-beta1)
 DE (Interleukin-12 receptor beta) (IL-12 receptor beta component).
 OS IL12RB1 OR IL12RB.
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=96025887; PubMed=7594587;
 RA Chua A.O., Wilkison V.L., Presky D.H., Gubler U.;
 RT "Cloning and characterization of a mouse IL-12 receptor-beta
 component.";
 RL J. Immunol. 155:4286-4294 (1995).
 RN [2]
 RP SUBUNIT.
 RX MEDLINE=97098510; PubMed=8943050;
 RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,
 RA Gately M.K., Gubler U.;
 RT "A functional interleukin 12 receptor complex is composed of two
 beta-type cytokine receptor subunits."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007 (1996).
 CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A
 CC LOW AFFINITY.
 CC -1- SUBUNIT: DIMER/OLIGOMER; DISULFIDE-LINKED. THE FUNCTIONAL HIGH
 CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
 CC IL12RB2.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U23922; AAA87457.1; -;
 DR MGD; MGI:104579; IL12RB1.
 DR InterPro; IPR003961; FN_III.

DR InterPro; IPR003529; Hemtopoptn_L_F2.
 DR Pfam; PF00041; fn3; 1.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; FALSE_NEG.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 738 INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN.
 FT DOMAIN 20 565 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 566 591 POTENTIAL.
 FT DOMAIN 592 738 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 142 142 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 152 258 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 259 359 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 360 465 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 467 553 FIBRONECTIN TYPE-III 5.
 FT DISULFID 53 63 BY SIMILARITY.
 FT CARBOHYD 50 50 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 130 130 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 368 368 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 374 374 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 477 477 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 738 AA; 81661 MW; 05D7AC306F1059CE CRC64;
 Query Match 3.5%; Score 122; DB 1; Length 738;
 Best Local Similarity 20.3%; Pred. No. 0.11;
 Matches 128; Conservative 61; Mismatches 183; Indels 260; Gaps 36;
 QY 38 CPLASHTVEPLPI-----SLAAPGPGSSPQSLGACVSGSTVPAVCASCQCQAVFNGASS 91
 Db 218 CPSENMAQEIQIRRRRLSSGAPGPGWDSMPVC---VP----- 254
 QY 92 TSCRNPKSLPHSSIGDTRCQHLRGSCCLVVTCLURAITF--PSPPTSPTRDFALKG 149
 Db 255 -----PEVLPOAKI--KFLVEPLNQG-----RRRLTMQGSQPLAVPE---GCRG 295
 QY 150 -PNLRIQRHGKVF-----PDWTHKGMEVGTGYNRRWQLSGGPFESPDLLPEAIRV 201
 Db 296 RPAQVAKHLVLRMLSCRCQAQTSKTVPGLKKLN-----LSGA-TYDLNLVLAKTFRGRS 349
 QY 202 TISSGPEVSVRLCHQWALECEELSSPYDVQKIVSGGHTVELPYEFLLP--CLCIEASYLQ 259
 Db 350 TI-----QKWLHPAQELTETRALNVSV-GGNMTSMQWAAQAPGTYTCLE----- 392
 QY 260 EDIVRRKKCFQSWPEAYGSDFWKSVHFTDYSOHTQVMWALTURCPKLLEAALCQRDWH 319
 Db 393 -----WQPW-----FOHNRNTH-----CTLIVPEEDPAKMWTHWS 424
 QY 320 TLCKDLPNATARESDGKVV---LEKVDLHPQLCFKQVPWFSEGNSS-----HVECPHQ 369
 Db 425 S-----KPTLEQECYRITVFASKPNKPNLMWATVLSSTYFGGNASRAGTTPHVSVRNQ 478
 QY 370 TGSILTS--WNVSMDTQAQQLILHFSRRMHATFSAAWSLPGLGQDTLVPVYTVSQV--- 423
 Db 479 TGDVSVEWTSASQLSTCPGVLTQVYVVRCAE--DGANE-----SENLVPP--TKQTVDLG 530
 QY 424 WRSDVQF-----AWKHLICP-----DVSYRHIGLLILAL-----LALLTLTG 460
 Db 531 LRSRVMYKQVADRATARLPQAWSH---PQRFSEVQISRLSIIFASIGSFASVLLVGSILG 587
 QY 461 VW-----LALTC----- 467
 Db 588 YIGLNRAWHLCPLPTPCGSTAVEFPFGSQGKQAWQMCNPEDPPEVLYPRDALVEMPGD 647
 QY 468 -----RRPQSGPGPA-----RPVLLHAADEAQR--RLVGALAEALLRAA----- 505

Db 648 RGDGTSPQAPEACALDRRL-----ETQRQVQVQALSEARRLGLAREDCPRGDLA 699
 QY 506 -----LGG---GRDIVDLWEGRHVARVGP 527
 Db 700 HVTLPGLGGVQTQASVLDLWRTHKTAEPGP 731

RESULT 4
 ID IL17_MOUSE STANDARD; PRT; 864 AA.
 AC Q60943;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-17 receptor precursor (IL-17 receptor).
 GN IL17R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymic lymphoma;
 RX MEDLINE=96111968; PubMed=8777726;
 RA Yao Z., Fanslow W.C., Seldin M.F., Rousseau A.M., Painter S.L.,
 RA Comeau M.R., Cohen J.I., Spriggs M.K.;
 RT "Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a
 RT novel cytokine receptor.";
 RL Immunity 3:811-821(1995).
 CC -!- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,
 CC suggesting that additional components are involved in IL17-induced
 CC signaling (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC
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 CC -----

DR EMBL; U31993; AAC52357.1; -;
 DR MGD; MGI:107399; Il17r.
 KW Receptor; Transmembrane; Signal; Glycoprotein.
 FT SIGNAL 1 31 POTENTIAL.
 FT CHAIN 32 864 INTERLEUKIN-17 RECEPTOR.
 FT DOMAIN 32 322 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 323 343 POTENTIAL.
 FT DOMAIN 344 864 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 809 814 POLY-GLU.
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 864 AA; 97807 MW; 343FD51AA687DA31 CRC64;

Query Match 3.5%; Score 121.5; DB 1; Length 864;
 Best Local Similarity 17.5%; Pred. No. 0.15;
 Matches 118; Conservative 97; Mismatches 182; Indels 277; Gaps 33;

QY 46 VLPISALAPGSPSPQSLGVCESGVPA-VCA--SICQVAVQVFNAGSSTWCNPKSLP 102
 Db 20 LLLNLVAP-GRASPRLL-----DFPAPVCAQEGLSRVN--STCLDDSWI-HPNLT 69
 QY 103 HSSSIDGTQCHLLRGSCCLVVTCLRRRAITPPSPPTPTDFALKGNRIQ--RHGV 160
 Db 70 -----PSSPKNIYI-----NLSVSTQHGL 90
 QY 161 FP-----DWT-----HKGNEVCT-----GYNRRVWVQLSGGPE 187

Db 91 VPVHLVWETLQTDASLYLLEGAELSVLQLNTNRLCKVKEQFLSMLOHHRKW-----R 143
 QY 188 FSPDLLPEARAIRVTISSGPEVSVRLCHO-----WALCEELSSPYDVQ 231
 Db 144 FSPS-----HFVDPGQGEYEVTVHILPKPIPDGDGNHKSIIIFVPCDESKMKMTTS 195
 QY 232 KIVSG-----GHTVELPYEFLPCLCTEASYLOED--TVRRKKCPQFQSWPEAYGSDFWKSV 285
 Db 196 CVSSGSLWDPNITVE-----TLDQHLRVDFTLWNSTPYQVLLS----- 236
 QY 286 HFTDYSOHTOMWMLTLRPLKLEAALCORHWHLTCKOLPNATARESOGVTVLEKVDLH 345
 Db 237 -FSDSENHSCFDVVKQIFAP-----RQEEPH-----QRANVTFTLSKFHW 276
 QY 346 POLCFKVPWFES-----FCNSSHVCEPQHOTGLTSMNVSMDTQAQQLILHFSRRMHTF 399
 Db 277 CHHHVQVFPFSSCLNDLCHAVTVCP----- 304
 QY 400 SAASWLPFGQDTLVP--PVYTVSQVWRSDVQFAWKHLLCPDVSYRHLGLL--ILALLALT 457
 Db 305 -----VISNTVPKPVADYIPLW-----VYGLTILAILLVGS 337
 QY 458 LGGVIALTR-----RPSG-----PGPARP--VLLHAADEAQRRLV 495
 Db 338 VIVLLICMTWRLSGADQEKHDDSKINGILPVADLTPLPLPKRWIVYSADHPIYVEV 397
 QY 496 GAAEELLRAALGGRDVIVDLWEGRHVARVGPPLWAAARTVAREQGVLLWS---GA 552
 Db 398 LKFAQLITAC--GTEVALDLEEQVISEGVWTVWSROKQEVESNKKIILCSRGTOA 455
 QY 553 DLRPVSG-----PDRAAPLALLHAAAPR-----LLLAYFSRLCAKGD 592
 Db 456 KWKAILGWAEPVQLRCDHWKPKAGDLFTAAMNMLPDFKRPACFGTVVVCYFSGICSERD 515
 QY 593 IPPPLRALPYRL 606
 Db 516 VPDLFNITSRYPLM 529

RESULT 5
 ID TPOR_HUMAN STANDARD; PRT; 635 AA.
 AC P40238;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thrombopoietin receptor precursor (TPO-R) (Myeloproliferative leukemia
 DE protein) (C-mpl) (CD110 antigen).
 GN MPL OR TPOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92302297; PubMed=1608974;
 RA Vigon I., Mornon J.-P., Cocault L., Mitjavila M.-T., Tambourin P.,
 RA Gisselbrecht S., Souvri M.;
 RT "Molecular cloning and characterization of MPL, the human homolog of
 RT the v-mpl oncogene: identification of a member of the hematopoietic
 RT growth factor receptor superfamily.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:5640-5644(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94292186; PubMed=8020956;
 RA Mignotte V., Vigon I., de Crevecoeur E., Romeo P.H., Lemarchandel V.,
 RA Chretien S.;
 RT "Structure and transcription of the human c-mpl gene (MPL).";
 RL Genomics 20:5-12(1994).
 CC -!- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY
 CC MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC NR3 SUBFAMILY.

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CC -----

DR EMBL; M68915; AAA39971.1; -

DR EMBL; U12644; AAA66067.1; -

DR PIR; A39596; A39596.

DR HSSP; P06401; IA28.

DR TRANSFAC; T04680; -

DR MGD; MGI:97567; Pqr.

DR InterPro; IPR000536; Hormone_rec_lig.

DR InterPro; IPR000128; Progesterone_receptor.

DR InterPro; IPR001628; Znf_C4steroid.

DR Pfam; PF00104; hormone_rec; 1.

DR Pfam; PF00105; zf-C4; 1.

DR Pfam; PF02161; Prog_receptor; 1.

DR PRINTS; PR00047; STROIDFINGER.

DR ProDom; PD000035; Znf_C4steroid; 1.

DR SMART; SM00430; HOL1; 1.

DR SMART; SM00399; Znf_C4; 1.

DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;

CC Zinc-finger; Steroid-binding.

FT DOMAIN 1 556 MODULATING, PRO-RICH.

FT DNA_BIND 557 622 NUCLEAR RECEPTOR-TYPE.

FT ZN_FING 557 577 C4-TYPE.

FT ZN_FING 593 617 C4-TYPE.

FT DOMAIN 671 923 STEROID-BINDING.

FT DOMAIN 184 188 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

CC SEQUENCE 923 AA; 99073 MW; 9415FIED343BEE3F CRC64;

Query Match 3.2%; Score 113.5; DB 1; Length 923;

Best Local Similarity 21.6%; Pred. No. 0.66;

Matches 98; Conservative 52; Mismatches 177; Indels 127; Gaps 24;

QY 23 SAGIGFRHLPHNTRCPPLASHTVEVLPIS-----LAAPGGSSPQSLGVCESGTVPAVCASI 78

DB 404 SAGASSTTFDP-----PLAPAPQAAPSRGPEAAVAGSSAAVSPASSG-----SAL 453

QY 79 CQQAQVFGASSTWCRNPKSLPHSSSTIGDTRCQHLRSGCCLVVTCLRRAITPPSPQ 138

DB 454 ECILYKA-----EAPPTQGSFAPLPCKPPAAASCLLPDRSL-----PAAPG 494

QY 139 TSPT-----RDFALKG-PNRIQRH-----GKVPDWTGKMGVEGTGYNRRWVQLSGGPE 187

DB 495 TAAAPAIYQPLGLNGLPQLGYQAAYLKDSLPPQVPPYLN-----YLRPDSEASQSPQ 546

QY 188 FSDLLPEARAIRVITSSGPEVSRVLRCHOWALECEBELSPYDVQKIVSGGHTVELPYEFL 247

DB 547 YGFDSLQ-----KICLICDEASG-CHVGVLTCG-SCKVFFKAMEGQNNY----- 591

QY 248 LPLCLTEASYLOEDTVRRKKCP-----FQSWPEAYSGDFWKSVFHFTDYS-QHTQVMYA 299

DB 592 ---LCAGRNDICVDKIRKNCPCACLRKCCQAGVGLGRKFKK-----FNKVRVMRTLDGVA 645

QY 300 LTLRCPKLKLEA-ALCORHWHTLCKDLNPATARESDGWVLEKVDLHP---QLCFKQVOPW 355

DB 646 LPQSVGLPNESQALSQRITFS-----PN-----QEIOLVPLNLNLSIEPD 687

QY 356 FSGNSSHVECPHQTSGLTSWVSMYMDTQAQQLLHFSRMRHATFSAAW-SLPGLGQDQL 413

DB 688 VIYAGHDNTKPDTSLSLTSLNQLGERLLSVV-----KWSKSLPGERNLHI 734

QY 414 VPPVTVSQVRSRVDQF--AWRHLLCPDYSYRHL 445

DB 735 DQDITLIQYSWNSLWVFGLGWR-----SYKHV 761

RESULT 7

Y173 HUMAN

ID Y173_HUMAN STANDARD; PRT; 1199 AA.

AC Q14679;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein KIAA0173.

GN KIAA0173.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Bone marrow;

RX MEDLINE=96281124; PubMed=8724849;

RA Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;

RT "Prediction of the coding sequences of unidentified human genes. V.

RT The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced by

RT analysis of cDNA clones from human cell line KG-1.";

RL DNA Res. 3:17-24(1996).

CC -!- SIMILARITY: CONTAINS 1 TTL DOMAIN.

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CC -----

DR EMBL; D79995; BAA11490.1; -

DR InterPro; IPR004344; Tub_tyr_lycase.

DR Pfam; PF03133; TTL; 1.

KW Hypothetical protein; Polymorphism.

FT DOMAIN 651 946 TTL.

FT VARIANT 418 418 R->H (IN DBSNP:2114664).

FT SEQUENCE 1199 AA; 133376 MW; 5306D5FA37431081 CRC64;

Query Match 3.2%; Score 113.5; DB 1; Length 1199;

Best Local Similarity 18.4%; Pred. No. 0.9;

Matches 102; Conservative 68; Mismatches 175; Indels 209; Gaps 27;

QY 16 IVIDLSDSAGIGFRHLPHNTRCPPLASHTVEVLPISLAAPG---GPSSPQSLGVCESGTVP 72

DB 419 ISIHLLASHASGLNH---NPAC-----ESVIDSAGFEGCKAPGPPPTLGI----- 462

QY 73 AVCASICQQAQVFGASSTWCRNPKSLPHS-----

DB 463 ---ANVATRLSSIQGQSEKERPEARELSDSDISSATDLPDQAEETDEELVDGL 519

QY 105 -----SSIGDTRCOHL-----LRGSCLVVT-----CLRRATFPS 135

DB 520 EDCSCSRNDEEEGDECSLSAVSPSESVAMISRSCEMLTKPLSNHKEKVRPALIYL 579

QY 136 PPQTSPTDRFA-----

DB 580 FPNVPTPIYGTDRDERVEKLPWEQRKLLRWKMSIVTPNIVKQITGRSHFKISKRNDDWL 639

QY 147 -----LKGPNLR-IQRHGKV--FPDWTGKMGVEGTGYNRRWVOLS-----GGPEFSF-- 190

DB 640 CWGHMKSPSFRSIREHQKLNHPG-----SFQIGR-KDRLWRNLRSRQSRFGKKEFSFP 694

QY 191 --DLIP-EARAIRVITSSGPE-----VSRLCHOWA-----LECEBELSS 226

DB 695 QSFILPDQAKLLRKAWESSRQKWIWKPPASARGIGIQVTHKWSQLPKRRPLLVQRYLHK 754

QY 227 PYDVQKIVSGGHTVELPYEFLPLCLCTEASV-----LOEDTVRRKKKCPQSWPEAYGS 279

DB 755 PY-----LISGS-----KFDLRIYVYVTSYDPLRIYLFSDGLVRFASCKYSPSMKSLGN 803

QY 280 DFWSVHTDYDYSQHTQVMALTLRCPLKLEAALCQRHWHHTLCKDLPNATARE---SDGW 336
 Db 804 KF---MHLTNS-----VNKNAEYQANADMACQGHK-ALKALWNLKSGVNSDA- 852
 QY 337 YVLEKV-DLHPQLCFKQVWFSGNSHVECHQTSGLTSWNVSMPTQAQQLL--HFSS 393
 Db 853 -IWEKTKDVVVKTIISSEPYVTSLLKMYVRRPYSCHELFGLDMLDENLKPWVLEVNISP 911
 QY 394 RMHATESAAMSLPG 407
 Db 912 SLHSSSPLDISIG 925

RESULT 8
 ID GSTR_RAT STANDARD; PRT; 452 AA.
 AC P30553;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Gastrin/cholecystokinin type B receptor (CKB-B receptor) (CKB-BR).
 GN CCKBR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92409582; PubMed=1528881;
 RA Wank S.A., Pisegna J.R., de Weerth A.;
 RT "Brain and gastrointestinal cholecystokinin receptor family:
 structure and functional expression";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:8691-8695(1992).
 CC -!- FUNCTION: RECEPTOR FOR GASTRIN AND CHOLECYSTOKININ. THE CKB-B
 RECEPTORS OCCUR THROUGHOUT THE CENTRAL NERVOUS SYSTEM WHERE THEY
 MODULATE ANXIETY, ANALGESIA, AROUSAL, AND NEUROLEPTIC ACTIVITY.
 CC THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS
 CC THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
 CC SYSTEM.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Parietal cells, pancreas, brain and various
 CC neoplastic tissues.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
 CC
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 CC
 CC EMBL: M99418; AAA40925.1; -;
 CC PIR: A46195; A46195.
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCR_Rhodpsn.
 CC PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 CC PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Lipoprotein; Palmitate.
 CC DOMAIN 1 57
 CC TRANSMEM 58 79
 CC DOMAIN 1 (POTENTIAL).
 CC TRANSMEM 80 87
 CC DOMAIN 2 (POTENTIAL).
 CC TRANSMEM 88 109
 CC DOMAIN 110 131
 CC TRANSMEM 132 150
 CC DOMAIN 151 170
 CC TRANSMEM 171 189
 CC TRANSMEM 190 219
 CC TRANSMEM 220 242
 CC DOMAIN 2 (POTENTIAL).
 CC TRANSMEM 243 266

FT DOMAIN 243 338
 FT TRANSMEM 339 360
 FT DOMAIN 361 378
 FT TRANSMEM 379 399
 FT DOMAIN 400 452
 FT CARBOHYD 7 7
 FT CARBOHYD 30 30
 FT CARBOHYD 36 36
 FT DISULFID 127 205
 FT LIPID 413 413
 FT DOMAIN 221 226
 SQ SEQUENCE 452 AA; 48956 MW; 006D811A6AA065C6 CRC64;
 Query Match 3.18; Score 107.5; DB 1; Length 452;
 Best Local Similarity 23.7%; Pred. No. 0.81; Indels 131; Gaps 16;
 Matches 75; Conservative 26; Mismatches 85;
 QY 391 FSSRMHA--TFSAAMSLPGLGQDTLVP--PVYTVSQV-----WRS-DVQFAWKHL 435
 Db 165 WQTRSHAARVILATWLLSGL--LMVPYVYTMVQVGPVLCMHWRPVSARVQVWTS-- 219
 QY 436 LCPDVSYRHGLLILALLALLTLLGVUAL-----TCRRPQ 471
 Db 220 -----VLLLLFFIPGVIAVAYGLISRELYLGLHFDGENDSETQSRARQ 266
 QY 472 SG-----PGP-----ARPVLLHLLHAADSEAQRRLVGALAEALLRAALGGGRDIVDLWEG 519
 Db 267 GGLPGGAAPGVHONGGCRPVTSVAGEDSD-----GCCVQLPRSL----- 307
 QY 520 RHVARVGPLWLAARTVAREOGTVLLLWSGADLRPVSGDPDRAAPLALLHAAPRLL 579
 Db 308 -----EMTLLTPPG-----PVGPGRPNQAKLLAKKRVV-RMLL 341
 QY 580 LLAVFSRLCAKGDIPPPRLALPRYLLRLDLRLRLDARFAPATSWGRGA----- 632
 Db 342 VIVLLFFLCL-----PVYSVNTWRAF-DGPGAQRLSGAPISFIHLLSVYACVNPV 395
 QY 633 ---RORROSRLELCSR 645
 Db 396 CFMHRFRQACIDTCAR 412

RESULT 9
 ID PRGR_RAT STANDARD; PRT; 923 AA.
 AC Q63445;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Progesterone receptor (PR).
 GN PR OR NR3C3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Placenta;
 RX MEDLINE=94130817; PubMed=8299566;
 RA Park-Sarge O.K., Mayo K.E.;
 RT "Regulation of the progesterone receptor gene by gonadotropins and
 RT cyclic adenosine 3',5'-monophosphate in rat granulosa cells";
 RL Endocrinology 134:709-718(1994).
 CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 CC NR3 SUBFAMILY.
 CC
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QY 389 LHFSRMHATFSAWSL-----PGLQDTLVPPVTVTSQWVRSDV 428
Db 505 MPHGG-PHSSFTYANMLPAMLCCKMGFAVLLVNYRGSTGFGQDSILSLPGNVGHQDVXDV 563
QY 429 QPAWKHL 436
Db 564 QPAVEQVL 571

RESULT 11
JAG2_RAT
ID JAG2_RAT STANDARD: PRT; 1202 AA.
AC P97607;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Jagged 2 (Jagged2) (fragment).
GN JAG2.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97103852; PubMed=8948600;
RA Shawber C., Boulter J., Lindsell C.E., Weinmaster G.;
RT "Jagged2: a serrate-like gene expressed during rat embryogenesis.";
RL Dev. Biol. 180:370-376(1996).
CC -|- FUNCTION: PUTATIVE NOTCH LIGAND INVOLVED IN THE MEDIATION OF NOTCH
CC SIGNALING. MAY HAVE A ROLE IN NEUROGENESIS IN THE PERIPHERAL
CC NERVOUS SYSTEM, LIMB DEVELOPMENT AND IN THE ADULT BRAIN.
CC -|- SURCELLULAR LOCATION: Type I membrane protein.
CC -|- DEVELOPMENTAL STAGE: AT STAGE E12.5 IT IS DETECTED IN DORSAL ROOT
CC GANGLIA, AER, AND SURFACE ECTODERM. AT E14.5, FOUND AS WELL IN
CC CRANIAL GANGLIA, THYMUS AND OLFACTORY EPITHELIA. AT E16.5, FOUND AS
CC WELL IN SALIVARY GLAND, TOOTH BUDS AND HAIR FOLLICLES.
CC -|- SIMILARITY: CONTAINS 16 EGF-LIKE DOMAINS.
CC -|- SIMILARITY: CONTAINS 1 DSL DOMAIN.
CC
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CC
CC EMBL; U70050; AAC52946.1; -;
CC HSSP; P00743; ICCF.
CC InterPro: IPR000152; Asx_hydroxyl.
CC InterPro: IPR001774; DSL.
CC InterPro: IPR000561; EGF-like.
CC InterPro: IPR000742; EGF_2.
CC InterPro: IPR001881; EGF_Ca.
CC InterPro: IPR001438; EGF_II.
CC InterPro: IPR000083; Fibractnl.
CC InterPro: IPR002049; Laminin_EGF.
CC InterPro: IPR001007; VWF_C.
CC Pfam; PF00008; EGF; 14.
CC Pfam; PF01414; DSL; 1.
CC PRINTS; PR00010; EGFBLD.
CC PRINTS; PR00011; EGFAMININ.
CC PRINTS; PR00012; FNYPPI.
CC SMART; SM00051; DSL; 1.
CC SMART; SM00179; EGF_Ca; 7.
CC SMART; SM00001; EGF_like; 8.
CC SMART; SM00214; VWC; 1.
CC PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_10.
CC PROSITE; PS00022; EGF_1; UNKNOWN_15.
CC PROSITE; PS01186; EGF_2; 11.
CC PROSITE; PS01187; EGF_Ca; 7.

Calcium-binding: EGF-like domain; Glycoprotein; Developmental protein;
Repeat: Transmembrane.
KW NON_PER 1
KW DOMAIN <1 1085
FT TRANSMEM 1086 1102 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 1103 1202 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 132 194 DSL.
FT DOMAIN 195 228 EGF-LIKE 1.
FT DOMAIN 229 259 EGF-LIKE 2.
FT DOMAIN 261 299 EGF-LIKE 3.
FT DOMAIN 301 337 EGF-LIKE 4.
FT DOMAIN 339 375 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 377 413 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 415 450 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 452 488 EGF-LIKE 8.
FT DOMAIN 490 527 EGF-LIKE 9.
FT DOMAIN 529 589 EGF-LIKE 10 (ATYPICAL).
FT DOMAIN 591 627 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 629 665 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 667 703 EGF-LIKE 13.
FT DOMAIN 706 742 EGF-LIKE 14.
FT DOMAIN 744 780 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 782 818 EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
FT DISULFID 199 210 BY SIMILARITY.
FT DISULFID 203 216 BY SIMILARITY.
FT DISULFID 218 227 BY SIMILARITY.
FT DISULFID 230 241 BY SIMILARITY.
FT DISULFID 236 247 BY SIMILARITY.
FT DISULFID 249 258 BY SIMILARITY.
FT DISULFID 265 277 BY SIMILARITY.
FT DISULFID 271 287 BY SIMILARITY.
FT DISULFID 289 298 BY SIMILARITY.
FT DISULFID 305 316 BY SIMILARITY.
FT DISULFID 310 325 BY SIMILARITY.
FT DISULFID 327 336 BY SIMILARITY.
FT DISULFID 343 354 BY SIMILARITY.
FT DISULFID 348 363 BY SIMILARITY.
FT DISULFID 365 374 BY SIMILARITY.
FT DISULFID 381 392 BY SIMILARITY.
FT DISULFID 386 401 BY SIMILARITY.
FT DISULFID 403 412 BY SIMILARITY.
FT DISULFID 419 429 BY SIMILARITY.
FT DISULFID 423 438 BY SIMILARITY.
FT DISULFID 440 449 BY SIMILARITY.
FT DISULFID 456 467 BY SIMILARITY.
FT DISULFID 461 476 BY SIMILARITY.
FT DISULFID 478 487 BY SIMILARITY.
FT DISULFID 495 506 BY SIMILARITY.
FT DISULFID 500 515 BY SIMILARITY.
FT DISULFID 517 526 BY SIMILARITY.
FT DISULFID 544 567 POTENTIAL.
FT DISULFID 561 577 POTENTIAL.
FT DISULFID 579 588 BY SIMILARITY.
FT DISULFID 595 606 BY SIMILARITY.
FT DISULFID 600 615 BY SIMILARITY.
FT DISULFID 617 626 BY SIMILARITY.
FT DISULFID 633 644 BY SIMILARITY.
FT DISULFID 638 653 BY SIMILARITY.
FT DISULFID 655 664 BY SIMILARITY.
FT DISULFID 671 682 BY SIMILARITY.
FT DISULFID 676 691 BY SIMILARITY.
FT DISULFID 693 702 BY SIMILARITY.
FT DISULFID 710 721 BY SIMILARITY.
FT DISULFID 715 730 BY SIMILARITY.
FT DISULFID 732 741 BY SIMILARITY.
FT DISULFID 748 759 BY SIMILARITY.
FT DISULFID 753 768 BY SIMILARITY.
FT DISULFID 770 779 BY SIMILARITY.
FT DISULFID 786 797 BY SIMILARITY.
FT DISULFID 791 806 BY SIMILARITY.
FT DISULFID 808 817 BY SIMILARITY.
SQ SEQUENCE 1202 AA; 129703 MW; 08CB44E5271FF8BE CRC64;


```

RESULT 13
PRGR_RABIT STANDARD; PRT; 930 AA.
P06186;
AC
DT DT 01-JAN-1988 (Rel. 06, Created)
DT DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Progesterone receptor (PR).
PGR OR NR3C3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
[1]
SEQUENCE FROM N.A.
MEDLINE=87067449; PubMed=3538016;
Loosfelt H., Atger M., Misträhi M., Guiochon-Mantel A., Meriel C.,
Legeat F., Benarous R., Milgrom E.;
"Cloning and sequence analysis of rabbit progesterone-receptor
complementary DNA.";
Proc. Natl. Acad. Sci. U.S.A. 83:9045-9049(1986).
CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
CC NR3 SUBFAMILY.
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-----
EMBL; M14547; AAA31443.1; -.
PIR; A25923; A25923.
HSP; P06401; 1A38.
TRANSFAC; T00697; -.
DR InterPro; IP0000536; Hormone_rec_lig.
DR InterPro; IPR000128; Progester_receptor.
DR InterPro; IPR001628; ZnF_C4steroid.
DR Pfam; PF001104; hormone_rec; 1.
DR Pfam; PF001105; zf-C4; 1.
DR Pfam; PF02161; Prog_receptor; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD0000035; ZnF_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
DR Zinc-finger; Steroid-binding.
KW DOMAIN
KW FT 1 565 MODULATING, PRO-RICH.
KW DNA_BIND 568 633 NUCLEAR RECEPTOR-TYPE.
KW ZN_FING 568 588 C4-TYPE.
KW ZN_FING 604 628 C4-TYPE.
KW DOMAIN 678 930 STEROID-BINDING.
KW DOMAIN 184 188 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
KW SEQUENCE 930 AA; 98666 MW; 644FF4C13BF2F883 CRC64;
Query Match 2.9%; Score 102; DB 1; Length 930;
Best Local Similarity 20.1%; Pred. No. 5;
Matches 90; Conservative 49; Mismatches 160; Indels 148; Gaps 21;
QY 51 LAAPGPGSPQSLGVGCESTVPAVCASICQVAQVNGASSTSWCRNPKSLPHSSIGDT 110
||||| ||||| : : : |||||
418 LAAPPPLPPLPPVSSRRPGEA-AVAAS- - - - -PGSASVS- - - - -SSSSSGST 458
db

```


Db 308 PSTPPEEPE---VIQVSLVPTLALLGLPIPRGIVEVMAELFSGGDSQPHSSALQA 364
 QY 376 WNVSMDTQAQQLLHFSS-----RWHATESAA-----WSLPLGQDTLPPVY 418
 Db 365 SALHLNAQVSRFLHYSAATODLQAKELHQNLFSKASADYQWLLQSPRAEATLPTVI 424
 QY 419 TVSQVMSDVQF-AWKHLICPDVSYRHLGLILALLALLTLLGVVIALTCRRPQSGP-P 476
 Db 425 AELQ-----QFLRGARACIE-SWARSISVRMAGGTALLAASCFICILLASQWATSPGFP 477
 QY 477 ARPVILLHADSQAQRLLVGAELRAALGGROVVDLWGRHVARVGP-LPWLWAAR 535
 Db 478 FCPLLLPVANG-----LVGAIA---YAGLLGTIELKLDLVILGAVAAVSSFLPLWKA- 528
 QY 536 TRVAREQGTVLLWVG-ADLRPVSGDPRAAPLLALL-----HAAPRPLL 579
 Db 529 -----WAGWGSKRPLATLFPPIPGVILLLLRLAVFFSDSVVAEARATPFL 575
 QY 580 LLAYFRLCA-----KGDIPPLRALPRYRLRLDRLRALDARPAEATSWG-RLGARQ 634
 Db 576 LGSFILLVQLHWEGQLLP-----KLLTMRPLGTSATNPPRHNGATVLRGI-- 625
 QY 635 RQSRLELCRL 646
 Db 626 ----GLLCTRL 633

RESULT 15

FBUB_SALTY STANDARD; PRT; 685 AA.
 AC 087656;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ferrichrome transport system permease protein fhuB (Ferrichrome uptake protein fhuB).
 GN FBUB OR STM0194.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2."
 RL Nature 413:852-856(2001).
 RN [2]
 RP SEQUENCE OF 467-685 FROM N.A.
 RC STRAIN-ATCC 14028S;
 RA Emmerth M., Goebel W., Miller S.I., Hueck C.J.;
 RT "Genomic subtraction identifies Salmonella typhimurium prophages and a novel fimbrial operon, stf, which are absent from S. typhi and E. coli";
 RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RL -!- FUNCTION: THIS IS ONE OF THE PROTEINS INVOLVED IN THE HIGH-AFFINITY TRANSPORT OF IRON(III)-FERRICHRONE INTO THE E. COLI CELL.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM PERMEASE FAMILY. FECCD SUBFAMILY.

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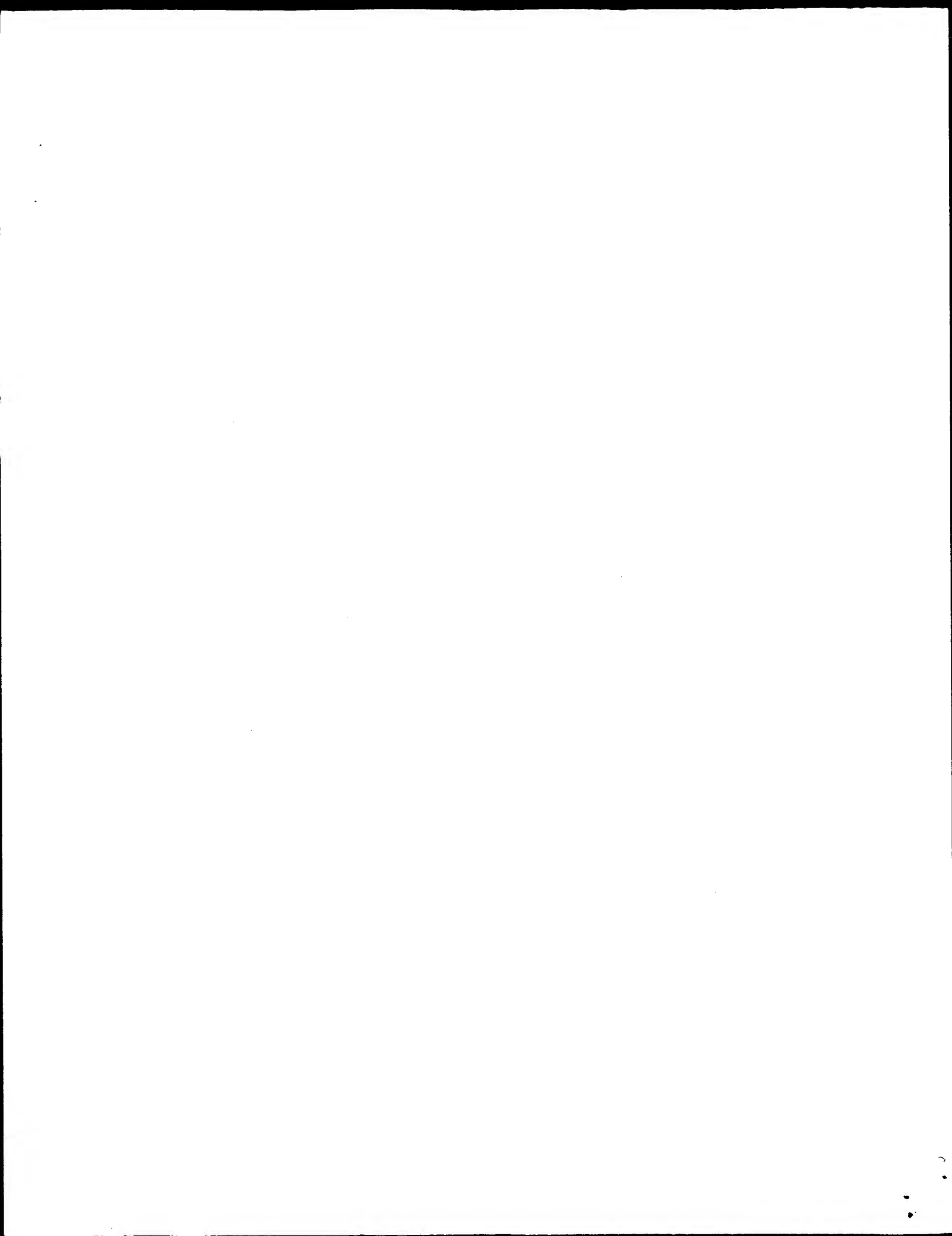
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 CC -----

DR EMBL; AE008703; AAL19158.1; -
 CC EMBL; AF093503; AAC64151.1; -
 DR StyGene; SG10641; fhuB.
 DR InterPro; IPR000515; BPD.transp.
 DR InterPro; IPR000522; FecCD.
 DR Pfam; PF01032; FecCD; 1.
 DR PRODOM; PD001557; FecCD; 1.
 DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; FALSE_NEG.
 KW Transport; Iron transport; Transmembrane; Inner membrane;
 KW Complete proteome.
 FT TRANSMEM 35 55 POTENTIAL.
 FT TRANSMEM 88 108 POTENTIAL.
 FT TRANSMEM 120 140 POTENTIAL.
 FT TRANSMEM 143 163 POTENTIAL.
 FT TRANSMEM 172 192 POTENTIAL.
 FT TRANSMEM 266 286 POTENTIAL.
 FT TRANSMEM 302 322 POTENTIAL.
 FT TRANSMEM 328 348 POTENTIAL.
 FT TRANSMEM 373 393 POTENTIAL.
 FT TRANSMEM 416 436 POTENTIAL.
 FT TRANSMEM 456 476 POTENTIAL.
 FT TRANSMEM 479 499 POTENTIAL.
 FT TRANSMEM 504 524 POTENTIAL.
 FT TRANSMEM 553 573 POTENTIAL.
 FT TRANSMEM 592 612 POTENTIAL.
 FT TRANSMEM 632 652 POTENTIAL.
 FT TRANSMEM 660 680 POTENTIAL.
 FT CONFLICT 470 479 NAGWLLPAG -> KPSGWYCLAE (IN REF. 2).
 FT CONFLICT 484 487 AAVL -> RRHW (IN REF. 2).
 FT CONFLICT 531 532 AE -> PK (IN REF. 2).
 SQ SEQUENCE 685 AA; 73203 MW; 547C0ACC551B353D CRC64;

Query Match 2.9%; Score 100.5; DB 1; Length 685;
 Best Local Similarity 22.2%; Pred. No. 4.5;
 Matches 93; Conservative 38; Mismatches 117; Indels 171; Gaps 19;

QY 345 HPQL-----CFKQVWFSEFGNSHVECPHOTGSLTSWNVMDTQAQQLLHFS----- 392
 Db 33 HPALLLLALFVAACWLTWNFS-VALPRSQWQAIAWSPDIDI-TEOMIFYSQLPRLAIS 90
 QY 393 -----SRMHATESAANSLPG----- 407
 Db 91 LLVAGLGLGVLFQOVLNRNPLAEPTTLGVATGAQGLGTVTLWAIFGALTTPQAALTGA 150
 QY 408 -----LGQDT-----LVPPVY-----TVSQ 422
 Db 151 CIVGALVFGVANGKRLSPVTLILAGLVVSLYCGAINQLLVIFHHQDLQSMFLWSTGTLTQ 210
 QY 423 VWRSDVQFAWKHL-----CPDVSYRHLGL-LILALLLTLGLVLA 464
 Db 211 TDWSGVQLWLPQLLGGVMTLLLLLRPMTLMGLDDGVARNLGLSLARLAALSIVLSA 270
 QY 465 LTCRRPQSGPGPARPVLLLHAADSEARLVGA---LAELLRAALGGG-----RDVLVDL 516
 Db 271 LLVN-----AVGIGFGLFAPLAKMLGARRLLARLMAPLIGALILWLSDQII-L 321
 QY 517 WGRHVARVGPLPWLWAARTVAREQGTVLLWVGADLRPVSGPDPRAAPLLA----- 569
 Db 322 W-----LTRV-----WNEVSTGVTALIGAPLLLLLPRLKMSAPDMNASDRVAERHVL 373
 QY 570 LLHAAPRPLLALLAFSRLC-----AKGDIPPLRALPRYRLRLDRLRALDA 618
 Db 374 AFVAGGALLLTLWTVALSFGDRAGHTWASGTL---LEELMPWR-----WPRILAALMA 425

Search completed: January 28, 2003, 09:29:42
 Job time : 22 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 28, 2003, 09:28:03 : Search time 37 Seconds

(without alignments)
3638.729 Million cell updates/sec

Title: US-09-863-818A-12

Perfect score: 3512

Sequence: 1 MGSSRLAALLPLLLIVIDL.....SPLELCSRLEREARLADLG 657

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.21.*

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.rodent.*
- 12: sp.virus.*
- 13: sp.vertebrate.*
- 14: sp.unclassified.*
- 15: sp.virus.*
- 16: sp.bacteriap.*
- 17: sp.archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1521.5	43.3	482	Q8TEC2	Q8tec2 homo sapien
2	1023	29.1	311	Q8R335	Q8r335 mus musculus
3	163.5	4.7	538	Q9BR97	Q9br97 homo sapien
4	159.5	4.5	567	Q99J43	Q99j43 mus musculus
5	122.5	3.5	474	Q73906	Q73906 gallus gall
6	113.5	3.2	1199	Q8W29	Q8w29 homo sapien
7	113.5	3.2	2864	Q59422	Q59422 hepatitis g
8	111.5	3.2	515	Q9RRK1	Q9rrk1 deinococcus
9	110.5	3.1	381	Q63095	Q63095 rattus norv
10	107	3.0	558	Q8KY53	Q8ky53 streptomyce
11	106.5	3.0	4268	Q8XYP2	Q8xyf2 ralsstonia s
12	106	3.0	428	Q88003	Q88003 bordetella
13	106	3.0	1463	Q70320	Q70320 cavia porce
14	105.5	3.0	7576	Q9ZGA4	Q9zga4 streptomyce
15	105	3.0	523	Q9HW81	Q9hw81 pseudomonas
16	105	3.0	587	Q8R0M9	Q8r0m9 mus musculus

17	105	3.0	2864	12	Q999T0	Q999t0 hepatitis g
18	104.5	3.0	847	11	Q9J364	Q9jj64 mus musculu
19	104	3.0	709	16	Q9RYK7	Q9ryk7 deinococcus
20	104	3.0	732	6	Q9TS46	Q9ts46 sus scrofa
21	103.5	2.9	401	16	Q9S221	Q9s221 streptomyce
22	103.5	2.9	498	16	Q9KXK2	Q9kxk2 streptomyce
23	102.5	2.9	606	16	Q9KY63	Q9ky63 streptomyce
24	102.5	2.9	1034	11	Q35888	Q35888 rattus norv
25	102.5	2.9	1456	2	Q9F636	Q9f636 stigmatella
26	102.5	2.9	2358	16	Q9LIV8	Q9lliv8 streptomyce
27	102	2.9	253	4	Q8W2B4	Q8wzb4 homo sapien
28	102	2.9	396	16	Q9EWX4	Q9ewx4 streptomyce
29	102	2.9	576	4	Q9Y2X4	Q9y2x4 homo sapien
30	102	2.9	576	4	Q9BRG2	Q9brg2 homo sapien
31	102	2.9	829	10	Q9SYA0	Q9sya0 arabidopsis
32	102	2.9	2035	16	Q8ZF24	Q8zfd2 yersinia pe
33	102	2.9	2041	2	Q9Z399	Q9z399 yersinia pe
34	101.5	2.9	513	2	Q8VPV8	Q8vpv8 synechococc
35	101.5	2.9	690	16	Q9LON2	Q9lon2 streptomyce
36	101.5	2.9	6315	2	Q9ADL6	Q9adl6 polyangium
37	101	2.9	428	2	Q45374	Q45374 bordetella
38	101	2.9	482	16	Q9I4A0	Q9i4a0 pseudomonas
39	101	2.9	906	16	Q9HX92	Q9hx92 pseudomonas
40	101	2.9	4809	2	Q93HH0	Q93hh0 streptomyce
41	100.5	2.9	392	4	Q9NT84	Q9nt84 homo sapien
42	100.5	2.9	1438	16	Q85739	Q85739 pseudomonas
43	100	2.8	1193	2	Q9Z5E0	Q9z5e0 rhodobacter
44	100	2.8	2864	12	Q9QEW5	Q9qew5 hepatitis g
45	99.5	2.8	1101	11	Q9JJU6	Q9jjj6 mus musculu

ALIGNMENTS

RESULT 1

Q8TEC2	Q8TEC2	PRELIMINARY;	PRT;	482 AA.
AC	Q8TEC2;			
DT	01-JUN-2002 (Tremblrel. 21, Created)			
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)			
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)			
DE	CDNA FLJ23658 fis, clone COLF3416.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=COLON MUCOSA;			
RA	Kawabata A., Hikiiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,			
RA	Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,			
RA	Tanaka T., Nakamura Y., Isogai T., Sugano S.;			
RT	"NEDO human cDNA sequencing project."			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK074238; BAB85028.1; ..			
SQ	SEQUENCE 482 AA; 54139 MW; 416455A73026B385 CRC64;			

Query Match	43.3%	Score 1521.5;	DB 4;	Length 482;
Best Local Similarity	69.7%;	Pred. No. 7.3e-113;		
Matches 313;	Conservative 15;	Mismatches 54;	Indels 67;	Gaps 10;
QY	1	MGSSRLAALLPLLLIVIDLSDSAGIGRFRHLPHNWTRCPPLASHTEVLPISLAAPGGPSP	60	
Db	1	MGSSRLAALLPLLLIVIDLSDSAGIGRFRHLPHNWTRCPPLASHTD-----	45	
QY	61	QSLGVCSGTPAVCASCCQVAQVFNCGASSTSCNRNPKSLPHSSIGDTRCOHLL----	116	
Db	46	-----DSFTGSSAYIPCRITWAL--FSTRKPCW---VRVWCHSR---CUCQHLLSGGS	89	
QY	117	-----RGSCCLVTCRLRAITF-----PSPQTS--PTRDFALKGNLRIQRHGKVPD	163	
Db	90	GLQRLGFLHLLVQKSKSSTFFRYRRHKNPAPAQRLKLLPRHLSEKSHHISIPS-----PD	144	

QY 164 WTHKGM-----EVGTGNRRWVQLSGGPEFSDLLPEARAIRVTISSGPEVSRL 213
 Db 145 ISHGLRSKRTQSPDWTESLPLRDSQRHGPEFSDLLPEARAIRVTISSGPEVSRL 204
 QY 214 CHOWALECELSPPYDVQKIVSGGHTVLPYFELLPCICIEASYLQEDTVRRKKCPFSW 273
 Db 205 CHOWALECELSPPYDVQKIVSGGHTVLPYFELLPCICIEASYLQEDTVRRKKCPFSW 264
 QY 274 PEAYGDFWKSVMHFTDYSOHTQVMWALTURCPKLEAALCQRHDWHTLCKDLPNATARES 333
 Db 265 PEAYGDFWKSVMHFTDYSOHTQVMWALTURCPKLEAALCQRHDWHTLCKDLPNATARES 324
 QY 334 DGWYLVLEKDLHPQLCFKVPWFSGNSHVECPHOTGSLTSWNVSMDFQAQQLILHFS 393
 Db 325 DGWYLVLEKDLHPQLCFK----FSGNSHVECPHOTGSLTSWNVSMDFQAQQLILHFS 380
 QY 394 RMHATSAWSLPGQLQDILVPPVTVSQ 422
 Db 381 RMHATSAWSLPGQLQDILVPPVTVSQ 409

RESULT 2

Q8R335 PRELIMINARY; PRT; 311 AA.
 AC Q8R335;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Hypothetical 34.1 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC026737; AAH26737.1;
 KW Hypothetical protein.
 SQ SEQUENCE 311 AA; 34102 MW; 00E706D6617CFF15 CRC64;

Query Match 29.1%; Score 1023; DB 11; Length 311;
 Best Local Similarity 71.3%; Pred. No. 2e-73;
 Matches 211; Conservative 17; Mismatches 44; Indels 24; Gaps 2;

QY 380 MDQAQQLILHFSRRMHTFSAWSLPLGQDILVPPVTVSQ-----422
 Db 1 MDQAQQLILHFSRRMHTFSAWSLPLGQDILVPPVTVSQ-----422
 QY 423 -----VWRSVQFAWKHLCPDVSYRHGLLILALLLTLGGVVALTCRRPQSGPP 476
 Db 61 QENCILVWRSVQFAWKHLCPDVSYRHGLLILALLLTLGGVVALTCRRPQSGPP 476
 QY 477 ARPVILLHAADSEARRLGALAEALLRAALGGGROVIDLWEGRHVARVGPLPWLWAART 536
 Db 121 TRPVLLHAADSEARRLGALAEALLRAALGGGROVIDLWEGRHVARVGPLPWLWAARE 180
 QY 537 RVAREQTVLLWAGADLPVSGPDPRAPLALLHAAPRPLLLAYFSRLCAKGDIPPP 596
 Db 181 RVAREQTVLLWAGADLPVSGPDPRAPLALLHAAPRPLLLAYFSRLCAKGDIPPP 596
 QY 597 LRALPYRLRLDLPRLLRALDAPFAEATSWGLRGARQRRLCSRLREAR 652
 Db 240 LRALPYRLRLDLPRLLRALDAPFAEATSWGLRGARQRRLCSRLREAR 652

RESULT 3

Q9BR97 PRELIMINARY; PRT; 538 AA.
 AC Q9BR97;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE Hypothetical 59.1 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=UTERUS;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006411; AAH06411.1;
 KW Hypothetical protein.
 SQ SEQUENCE 538 AA; 59127 MW; 65E6344DA6A5AFD2 CRC64;

Query Match 4.7%; Score 163.5; DB 4; Length 538;
 Best Local Similarity 22.7%; Pred. No. 0.0001;
 Matches 128; Conservative 56; Mismatches 184; Indels 197; Gaps 32;

QY 36 TRCPPLASHTVLPISLAAPGGSPQSL-----GVCESGTPAVCACTCCQVAVFNQASS 91
 Db 78 TDCDLCLR---VAVHLAVHGHWEPEDEKFGGAADSGVEEPRNASLQAQVLSFQ-AYP 133
 QY 92 TSWC-----RNPKSL-PHSSSIGDTRCQHLRLGSCCLVVTCLRAITFPSPPTSPTRDF 145
 Db 134 TARCVLLEVOVPAALVDFGQSVGS-----VYDCFEAAL-----GSEVRIM 174
 QY 146 ALKGPNLRIQ-RHGKVPF-----DWTHKGMVGT-----GYNRRWVQLSGGPEFS 189
 Db 175 SYTPRYKELNHTQQLPALPWLNVADGNVHLVNLVSEHQHGLSLYWNQVQGPVK-- 232
 QY 190 FDLLEPRAIRIVTISSEPEVSVRICHOWALECELSPPYDVQKIVSGGHTVLPYFLLP 249
 Db 233 -----PRW-----HKNLTGPQITLNLNHTDLVP 254
 QY 250 CLCIEASYLQEDTVRRKKCPQSWPEAYGDFWKSVMHFTDYSOHTQVMWALT- 303
 Db 255 CLCIVVPLEPDSVRTNICPFEDPRAH-QNLWQAAR-----LRLTLQSWLLDA 303
 QY 304 -CPKLEAALCQRHDWHTLCKDL-----PNATARES DGWYLVLEKVDL--HPQLCFKVP 354
 Db 304 PCSLFAEAALCWRAPGGDPQCPPLVPLSWENVYDK-----VLEFPLKGNLVCVQ-- 356
 QY 355 WFSFGNSH-----VEC--PHOTGSLTSWNVSMDFQAQQLILHFSRRMHTF--SAWSL 406
 Db 357 -----NSSEKLQLOECLWADSLGPLKDDVLLLETRGPQ-----DNRSICALPEPGCTSLP 406
 QY 407 G-----LGODTLVPPVTVS-----QVWRSVQFAWKHLCPDVSYRHGLLIL 450
 Db 407 SKASTRAARLGE-----YLLQDLQSGCQLQWDDDLGALW---ACPMKYIHKRWALV 456
 QY 451 ALLALLTLGGVVALTCRRPQSGPPARPVLLLHAADSEARRLVGAALAEALLRA----- 504
 Db 457 WLACL--LFAAALS-----ILLKKDHAKGWLRL---LKQDVRSGGEWEQ 497
 QY 505 ALGGRDVIVDLWEGRHVARVGPLP 529
 Db 498 ALGGGPP-----PCSQACASSPLP 516

RESULT 4

Q99J43 PRELIMINARY; PRT; 567 AA.
 AC Q99J43;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Hypothetical 62.8 kDa protein.
 GN ILI7RL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]


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DR EMBL; BC021707; AAH21707.1; -.
DR InterPro; IPR004344; Tub_tyr_lygase.
DR Pfam; PF03133; TTL; 1.
KW Hypothetical protein.
SQ SEQUENCE 1199 AA; 133366 MW; 10F3C75DA0A030B1 CRC64;

Query Match
Best Local Similarity 3.2%; Score 113.5; DB 4; Length 1199;
Matches 102; Conservative 68; Mismatches 175; Indels 209; Gaps 27;

QY 16 IVIDLSAGIGFRLPHWNTRCPILASHTVEPLVPLSLAPG---GPSSPQSLGVCESGTPV 72
Db 419 ISIHLLASHASLNH---NPAC-----ESVIDSAFGEKAGPPPPQTLGI----- 462
QY 73 AVCASICQVAOVFNAGSSTWCRNPKSLPHS----- 104
Db 463 ---ANVATRLSIQIQSEKERPEARELSDSDRDISSATLDLPDOAETDEELVDLSL 519
QY 105 -----SSIGTRCOHL-----LRGSCCLVVT-----CLRRAITFPS 135
Db 520 EDCGCRDENEEBEGDSECSLSAVSPSESVAMISRSCMEILTKPLSNHEKVVRPALIYSL 579
QY 136 PQTSTPTDFA----- 146
Db 580 FPNVPTTYFGTRDERVEKLPWEQRKLLRWKMSVTPNIVKQITGRSHFKISKRNDDWL 639
QY 147 -----LKGPNLR-IORHGKV--FPDWTGKMGVEGFGYNNRWVOLS-----GGPEFGF-- 190
Db 640 CWGHHMKSPFSFRIEHOQKLNHFG---SFQIGR-KDRLWRNLRMSRFGKKEFFSFP 694
QY 191 --DLLP-EARAIRVTSSGPE-----VSVRLCHQW-----LECEELSS 226
Db 695 QSFILPQDAKLLRWKAWSSSRQKWIWPKPASARGIGIQVHKWSQLPKRRPLLYQVRLHK 754
QY 227 PYDVQKIVSGGHTVLPVEFLPLCLICIASY-----LQEDTVRRKKCPQSPWEAYGS 279
Db 755 PY-----LISGS-----KFDLRIYVYVTSYDPLRIYLFSDGLVRFASCKYSPSMKSLGN 803
QY 280 DRFKSVHVTDSQHTQVMYALTLRCPLEAALCORHDWHTLCRDLPNATARE---SDGW 336
Db 804 KF---MHLTNY-----VNKNNAEYQANADEMACOGHKW---ALKALNNYLSQKGVNSDS- 852
QY 337 YVLEKV-DLHPQLCRKVPWFSGNSHVECPHQGTSLTSWNSVMDTQAOQLILH-FHSS 393
Db 853 -IWEKIDKVVVKTIISSEFYVTSLLKMYVRRPYSCHELFDFDILMDENLKPWVLEVNISP 911
QY 394 RMHATFSAWSLPG 407
Db 912 SUHSSPLDISIKG 925

RESULT 7
Q69422 PRELIMINARY; PRT; 2864 AA.
AC Q69422;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Genome polyprotein [Contains: envelope glycoprotein E1 (GP32)
DE (GP35)]
OS Hepatitis GB virus B.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae.
OX NCBI_TaxID=39113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95241511; PubMed=7724574;
RA Simons J.N., Pilot-Natlas T.J., Leary T.P., Dawson G.J., Desai S.M.,
RA Schlauder G.G., Muerhoef A.S., Erker J.C., Buijk S.L., Chalmers M.L.,
RA van Sant C.L., Mushawar I.K.;
RT "Identification of two flavivirus-like genomes in the GB hepatitis
RT agent.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:3401-3405(1995).
RN [2]

RP SEQUENCE FROM N.A.
RA Simons J.N.;
RA Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
DR EMBL; U22304; AAC54059.1; -.
DR HSSP; P27958; 1HEI.
DR MEROPS; S29.002; -.
DR MEROPS; U39.001; -.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR002521; HCV_core.
DR InterPro; IPR002519; HCV_env.
DR InterPro; IPR002518; HCV_NS2.
DR InterPro; IPR004109; HCV_NS3.
DR InterPro; IPR000745; HCV_NS4a.
DR InterPro; IPR001490; HCV_NS4b.
DR InterPro; IPR002868; HCV_NS5a.
DR InterPro; IPR002166; HCV_RdRP.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01538; HCV_NS2; 1.
DR Pfam; PF02907; HCV_NS3; 1.
DR Pfam; PF01006; HCV_NS4a; 1.
DR Pfam; PF01001; HCV_NS4b; 1.
DR Pfam; PF01506; HCV_NS5a; 1.
DR Pfam; PF00998; HCV_RdRP; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; RNA-directed RNA polymerase; Transmembrane.
SQ SEQUENCE 2864 AA; 312701 MW; 5F5A7D8FAF0CDE81 CRC64;

Query Match
Best Local Similarity 23.9%; Pred. No. 7.9;
Matches 104; Conservative 48; Mismatches 170; Indels 113; Gaps 25;

QY 232 KIYSGGHTVLPVEFLPLCLICIASYLOEDTVRRKKCPQSPWEAYGSDFWKSVHFTDYS 291
Db 353 KVTGCSIAEFCPLMIPCPC--HSLSEN-VSEICYSPKTRPTVLENNISWYPT 409
QY 292 QHTQVMYALTLRCPLEA---ALCORHDWHTLCRDLPNATARESDGWVYKVDLHPQL 348
Db 410 -----IPGARGCMVKFNNTWGCGRIRNVPVSYCTMGTDVAVNDTRNTY-----EA 454
QY 349 CFKVPWFSGNSHVECPHQGTSLTSWNSVMDTQAOQLILH-FHSS 393
Db 455 C-GVTPMLTAWINGSALKAILQYPGCKEMFKPHNMMSGHLFYEGSDTP-----IVFYD 509
QY 394 RMHATF--SAWS--LPGLGQDITLVPV-----YTVSVMRSDVQ-----FAWKHL 435
Db 510 PVNSTLLPPERWARLPG-----TPVVRGSLQVPGGFYSDVKDLATGLITKDKAKNY 563
QY 436 LCPDVSYRHLGLLIL-----ALLALLLLG---VVALTCRRP-----QSGGPPARPVL 481
Db 564 ---QVLYSATGALSGLTGVTTKAVVLILLGLCGSKYLILAYLCYLSLCFGRASGYLRPVL 620
QY 482 ---LLHAADSEAQORRLVAGALA-----ELLRAALGGGRDVIDLWEGRHVARVG 526
Db 621 PSOSYLOAGWDVLSKAQVAPFALIFFICCYLRCLRRLRYAALLGVFVPMAGLPLTFFVAAA 680
QY 527 PLP-WLWAARTVRAREOGTVLLWSGADLRP-----VSGDPDRAAPLIALIH-AAPRPLLL 580
Db 681 AQPDYDWWVRLVAG-----LVLWAGDRGPRIALLVGPPPLVA-LTLLHLATPAS--- 731
QY 581 LAYFSRLCAKGDIPP 595
Db 732 -AFDETIIGLTIPP 745

RESULT 8
Q9RRK1 PRELIMINARY; PRT; 515 AA.
AC Q9RRK1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

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Nature 417:141-147(2002).
 EMBL; AL356832; CAB92674.1; -.
 SQ SEQUENCE 558 AA; 55368 MW; 38A2BC41EF030EE7 CRC64;

Query Match 3.0%; Score 107; DB 16; Length 558;
 Best Local Similarity 26.3%; Pred. No. 3.3;
 Matches 74; Conservative 28; Mismatches 93; Indels 86; Gaps 13;

QY 405 LPGLGQDPLVP-PVYTVSQVWRSVQFAWKHLLCPDVSYRHGLGILLIALLALLLLGW- 462
 DB 1 MAGVLTQTTARPAFLSLTRWD-----RSPGLAAGLLGGVAAVLGLAACALVT 51
 QY 463 -LALTCRRPQSGPAPRVLLIHAADSAORRLVGAELRAALRAALGGGRDVIIDLWEGRH 521
 DB 52 LLIWISSPYDSGPGA-----LHVA---AALWLAHGAELVRADTLSTGP----- 93
 QY 522 VARVGPLP-----WLWAARTVAREQGTIVLLWSGADLRPVSGDDPRAAPLLALLHA 573
 DB 94 -APVGVTPLELLFLLPVLLHRAARDATDPDGGVGAVGA--APKAGPGCARPAMWASAPDT 150
 QY 574 APRPL-----LLAYFS-----RLCAKGD-----IPPLRAL----- 600
 DB 151 GPPVSVARVMTGVVGLVAVGPVLLTAQGGALRPASAWAAVCLPLVAMGAAGAGWTA 210
 QY 601 -----PRYLRLDLPRLLRALDARPAEATSWGLGARQR 635
 DB 211 FGRPGGPVGRALRVLPKRLRELWPEPA-----RLGAATR 245

RESULT 11
 Q8XYF2 PRELIMINARY; PRT; 4268 AA.
 AC Q8XYF2
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Probable polyketide synthase protein.
 GN RSC1806 OR RS04228.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GMI1000;
 RX MEDLINE=21681879; PubMed=118233852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 Chardier M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
 Weissenbach J., Boucher C.A.;
 RA "Genome sequence of the plant pathogen Ralstonia solanacearum.";
 RL Nature 415:437-502(2002).
 DR EMBL; AL646066; CADI5508.1; -.
 DR InterPro; IPR001227; Ac transferase.
 DR InterPro; IPR000873; AMP-bind.
 DR InterPro; IPR001242; Condensatn.
 DR InterPro; IPR000794; Ketoacyl-synt.
 DR InterPro; IPR001601; Methyltransf.
 DR InterPro; IPR003880; Ppanne-attach.
 DR InterPro; IPR000408; Reg_chir_condens.
 DR InterPro; IPR000051; SAM_bind.
 DR Pfam; PF00698; Acyl_transf; 1.
 DR Pfam; PF00501; AMP-binding; 2.
 DR Pfam; PF00668; Condensation; 2.
 DR Pfam; PF00109; ketoacyl-synt; 1.
 DR Pfam; PF02801; ketoacyl-synt_C; 1.
 DR Pfam; PF00550; pp-binding; 4.
 DR PRINTS; PR00154; AMPBINDING.
 DR PROSITE; PS00075; ACP_DOMAIN; 4.
 DR PROSITE; PS00455; AMP_BINDING; 2.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.

DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_2.
 DR PROSITE; PS00626; RCC1_2; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 4268 AA; 457109 MW; 960E31222B7A30DF CRC64;

Query Match 3.0%; Score 106.5; DB 16; Length 4268;
 Best Local Similarity 20.5%; Pred. No. 47;
 Matches 98; Conservative 39; Mismatches 151; Indels 189; Gaps 21;

QY 305 PKLEAALCORHDHHTLCKDLPNATARESDGWYVLEKVDLHQLCFKVPWFSGNSHV 364
 DB 3751 PNGMQRVLPVPDYRIACODLRCGAAEVESEWLEIVRLEL-----SH- 3792
 QY 365 ECPHQTSLSLTSNV-----SMDTQAQQLI-----LHFSRMHATFSAAWSLPLGQDPL 413
 DB 3793 EAPDTTG-----WPLFTVRAARMSDTRIRLIFSLDLNLCVDCGRSMRTLLAEWSRLAREPGTV 3848
 QY 414 VPPV-----YTVS-QVWR-----SDVQFA 431
 DB 3849 LPPLSATFRDYVLLTEQLALRPSYQSRSLRYWHDKLTLPAPALPRGRHAADAVSPHFT 3908
 QY 432 WKHLLCPDVSYRHL-----GLLIALLALLTLLGVVLTATC-----RRPOS 472
 DB 3909 RREASLPFAQWQALQRAAQAQGVTVNAL--LAAAYGEVLANNWCATPFTLNTLTFNRPV 3966
 QY 473 GP-----GPAREVLLL-----HAADSEAQRRL-----VGALAEILLRAA--- 505
 DB 3967 HPQIDALVGDFTSLLVLLAFDGTAAALGFAQALAMQRIWADLEHMQVSAVRVLEAARN 4026
 QY 506 -----LGGGRDVIVDLWEGRHIVARVGLPWLWAAARTVAREQGTIVLL 548
 DB 4027 RRLDPVAMPVVFVTSGLGVAGDGDSEMD-WLGHFVYGVSTPQWIDQ-QVVERNGALVTN 4084
 QY 549 WSGADL-----RPVSGPDPR-----AAPILLALHAA 574
 DB 4085 WDAVDTLFPDGLDDMFPRAYRDLILLRADOPEAMQRPVGGDLPASWPVAAPAASAAQA 4144
 QY 575 PR-----PLLLL-----AFYSRLCARGDIPPPRALPRYRLRLDRLPRLRALDA 618
 DB 4145 PQADAGPALAVDDAILATVTRGMLGALTGRGELPVQVNFELGATSLDLIRLRLQQLWA 4201

RESULT 12
 O88003 PRELIMINARY; PRT; 428 AA.
 AC O88003
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Putative 3-deoxy-D-manno-octulosonic-acid transferase.
 GN WAAA.
 OS Bordetella bronchiseptica (Alcaligenes bronchisepticaus).
 OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 OC Bordetella.
 OX NCBI_TaxID=518;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CN7635E;
 RX MEDLINE=99346157; PubMed=10417135;
 RA Preston A., Allen A.G., Cadisch J., Thomas R., Stevens K.,
 Charcher C.M., Badcock K.L., Parkhill J., Barrrell B., Maskell D.J.;
 RA "Genetic Basis for Lipopolysaccharide O-Antigen Biosynthesis in
 RT Bordetella";
 RL Infect. Immun. 67:3763-3767(1999).
 DR EMBL; AJ007747; CAA07673.1; -.
 DR InterPro; IPR001296; Glycos.transf_1.
 DR Pfam; PF00534; Glycos.transf_1; 1.
 KW Transferase.
 SQ SEQUENCE 428 AA; 45386 MW; 9F3B59629D92D5E1 CRC64;

Query Match 3.0%; Score 106; DB 2; Length 428;
 Best Local Similarity 24.6%; Pred. No. 2.9;
 Matches 70; Conservative 22; Mismatches 91; Indels 102; Gaps 12;

QY 423 VMSDVQFAWKHLICPDVSYRHL-----GLLILA-----LLALLTLGGVVLALTCRRP 470
 Db 103 IGRCLQOAMLPDYDFGATRRFLARHAPRCGLLIEREVNLLAARAQGV-----153
 QY 471 QSGPGPARPVLLHAADEAQRRLVGAELRAALGG-GRDIVDLWEGRRHVARVGLP 529
 Db 154 -----PMALVSARFSASSLRQAGWLQALREALAGLGRVLAQTDGARCQCAGANA 205
 QY 530 W-----LWAATRVARQGTVLLWSGADLRPV-----SGPDPRAAPLLALL 571
 Db 206 YTVTGSLLKFDVALPEAQLRVGH-----AWAGATGRPVIALASTREGEDAMFIEAIGAL 258
 QY 572 H-----AAPRLPLL-----LAFSLRCLCAKGDIPPLRALPRYELLR 607
 Db 259 QAHRAATPRPLLIPRPHORFDEAAALQOAGLAVARRSAGSGEGCPHIDVL-----311
 QY 608 DLPRLLRALDARPPAEAT-----SWGRLGARQRQRSLRLECS 644
 Db 312 ----LGDTLGEMPFFYAAADVAIVGGSFARLGG-----QNLEIACA 348
 RESULT 13
 ID 070320 PRELIMINARY; PRT; 1463 AA.
 AC 070320;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Phospholipase B.
 GN PLB.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CR1:(BFA)BR; TISSUE=INTESTINE;
 RX MEDLINE=98256256; PubMed=9593672;
 RA Delagebeaudet C., Gassama-Diagne A., Nauze M., Ragab A., Li R.Y.,
 Capdevielle J., Ferrara P., Fauvel J., Chap H.;
 RT "Ectopic Epididymal Expression of Guinea Pig Intestinal Phospholipase
 B. Possible role in sperm maturation and activation by limited
 proteolytic digestion.";
 RL J. Biol. Chem. 273:13407-13414(1998).
 DR EMBL: AF045454; AAC40129.1;
 DR InterPro: IPR001087; Lipase_GDSL.
 DR InterPro: IPR003662; sub_transporter.
 DR Pfam: PF00657; Lipase_GDSL; 3.
 DR PROSITE: PS01098; LIPASE_GDSL_SER; 2.
 DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
 SQ SEQUENCE 1463 AA; 162175 MW; 101C4969815F24B1 CRC64;

Query Match 3.0%; Score 106; DB 11; Length 1463;
 Best Local Similarity 20.4%; Pred. No. 13;
 Matches 84; Conservative 46; Mismatches 136; Indels 146; Gaps 20;

QY 143 RFALKGNRIORHGKVFDPDTHKMEVGTGNRRWVQLSGGPFSDLLPEARIRVT 202
 Db 444 REF---NPSL-----KGFSTGTGKANSVGAFNNQAVAGARAG-----DLIPOARTLVLDL 489
 QY 203 ISSGPEVSVRLCHQWALECEELSSPYDVQKIVS---GGHVELPYEFLLPCLIEASYLQ 259
 Db 490 MKN---HTSINFEEDW-----KLIITVFIGNDL-----514
 QY 260 EDTVRRKKCPFSQWPEAYGSDFKWSVHFDT-----YSQHTQVMVMTLIR 303
 Db 515 -----CDFCSDPVNTSP-----NFTDNIRQALDILHAEVPRAFNVMVKVLIQVNL 561
 QY 304 -----CPLKEALCORHWHLCKDLPNATRESQGVVLEK-----341
 Db 562 ELYKDSRVSCPRLILNLCR-----CVLLPDNDSTELSLIDINKYQERTHQLIESG 614

QY 342 -VDLHPQLCFKVPWFSGNSSHVECPHOTGSLTSMNVSMDFQAQOQLILHSSRMHA-TF 399
 Db 615 RYDTRDFTVVLQPF-----EKVDIPK-----TSEGLPDNTSFAPDCFHSSKTHARAA 664
 QY 400 SAWS--LPLGQDQTLVPPVTVSVQWRSQVFAWKHLICPDVSYRHLGLLITALLALIT 457
 Db 665 SALKNMKEPVQOK-----TQNNFENSID-----IICPNQAFPLYSTYKNG-----706
 QY 458 LIGVVALTCRRPQSGPGPARPVLLHAADEAQRRLVGAELRAALGG 509
 Db 707 IEHGHTWLTCTRTPTSPASPTSVHALRPADV-----RVVAALGDSLITAGSGIG 754
 RESULT 14
 ID Q9ZGA4 PRELIMINARY; PRT; 7576 AA.
 AC Q9ZGA4;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE FK506 polyketide synthase.
 GN FKBB.
 OS Streptomyces sp. MA6548.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=82632;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=MA6548;
 RX MEDLINE=98451508; PubMed=9780228;
 RA Motamedi H., Shafiee A.;
 RT "The biosynthetic gene cluster for the macrolactone ring of the
 immunosuppressant FK506.";
 RL Eur. J. Biochem. 256:528-534(1998).
 DR EMBL: AF082100; AAC68815.1;
 DR HSP: P08659; 1LC1.
 DR InterPro: IPR001227; AC_transferase.
 DR InterPro: IPR002085; Adh_zn_family.
 DR InterPro: IPR000873; AMP_bind.
 DR InterPro: IPR000292; For/Nit_trnsprt.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR InterPro: IPR000794; Ketoacyl-synt.
 DR InterPro: IPR003880; Peantne_attach.
 DR InterPro: IPR003862; sub_transporter.
 DR Pfam: PF00698; Acyl_transf; 4.
 DR Pfam: PF00107; adh_zinc; 1.
 DR Pfam: PF00501; AMP-binding; 1.
 DR Pfam: PF00109; ketoacyl-synt; 4.
 DR Pfam: PF02801; ketoacyl-synt_C; 4.
 DR Pfam: PF00550; pp-binding; 5.
 DR PROSITE: PS00075; ACP_DOMAIN; 5.
 DR PROSITE: PS00455; AMP_BINDING; 1.
 DR PROSITE: PS01005; FORMATE_NITRITE_TP_1; UNKNOWN_1.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_4.
 DR PROSITE: PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
 KW Phosphopantetheine; Transferase.
 SQ SEQUENCE 7576 AA; 790105 MW; 49765AB9E66DD96 CRC64;

Query Match 3.0%; Score 105.5; DB 2; Length 7576;
 Best Local Similarity 20.6%; Pred. No. 1.2e+02;
 Matches 140; Conservative 62; Mismatches 199; Indels 279; Gaps 35;

QY 16 IVIDLSDSAGIFRHLPHW-----NTRCPLASHT-----EVLPIISLAAPG 55
 Db 5190 VAVDPEVIGARPTDPLHPTYPFFERTVWLSRAGDAAPAGQLPVAHPVLTAAVMYPG 5249
 QY 56 -----GPSSQSLGVCESGTVPAVCASICQVAVNGASSTSWCRNP-----KSL 101
 Db 5250 TGDVLVTGRVETDPLATVRHPGAARAVLLDLRSRA---TKRAAAPRRSPWTPRSAL 5306
 QY 102 PHSSSIGDTRCQHLRLGSCCLVVTCL-----RRAITFPSPQTSPTDRFALKGNLRIO 155

Db 5307 PQS-----GGIALSVTVAAPGCGRRRAVAVHARPGTG----- 5338
Qy 156 RUGKVPFWTHKGMVGTGYNRRWQLSCGPFESFDLLPEARAIRVTISSGPEVSVRLCH 215
Db 5339 -----EHTAGILARVARV-----ASAVPETSPWPPATAR----- 5371
Qy 216 QWALECEELSSPYDV-----OKTVSGGHT--VELPYEFLPCLCIEASYLQEDTVRRKKCP 269
Db 5372 -----PFDVGLADRLARAGHTDGPALPR----- 5396
Qy 270 FOSWPEAYGDFWKSVEHFDYSQHTQMVNALTLCPLKLEALCORHDMHTLCKDLPNAT 329
Db 5397 RAAWAD-----DDAVHAEVALA-----DEQHAD 5419
Qy 330 ARESDGWVLEKVDLHPQLCFKVPWFSEFGNSHVECP-----HQTG-----SLTS 375
Db 5420 A-----ERYGLHPALLGAALALAGE-----ADLPFAFDVVRVHATGATTVRVAVTA 5466
Qy 376 WNVSMDTQAQQLILHFSSRMHATFSAANSLPGLGQDTL-----VPPVTVTSQVWRSVDQF 430
Db 5467 TGIHLADEFGSPVAVGVARRRPLVEGAVPGLLRPDIAETAELEPPT-TATGGLDLP-- 5523
Qy 431 AMKHLCPDV-----SYRHIGLILALL-ALLT---LLGVVLTALTCRRPQS 472
Db 5524 -----VPPDWILPAHGTGGGPGTETDLGARVLAALRSFLTDDRYADAVLAV-----HT 5573
Qy 473 GPG--PARPVLLHRAADSEAORRLVCAAE-----LLRAALGGGRDVIQDLWEGRHVAR 524
Db 5574 GPGAPAAAGLVRTAQAEBHPRIVVDAEPDTPAFLAAAAGLGEPOVV-LREGRAYAR 5632
Qy 525 -----VGPLFWLWAARTRVAREOGTVLLWSGADLRPVSGPDRAAPLLA---LLHAA 574
Db 5633 RUTPAVPSGDAPDL-----DPDGTVL-----ITGSGTLAGIARHLVGHYG 5674
Qy 575 PRPLLLLYFSLCAKGDIP 594
Db 5675 VRRLLML---SRGGTASDVP 5691

RESULT 15

Q9HW81 PRELIMINARY; PRT; 523 AA.
AC Q9HW81;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical protein PA4320.
GN PA4320.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Miziouchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen";
RL Nature 406:959-964(2000).
DR EMBL; AE004848; AAG07708.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 523 AA; 59671 MW; 56B9F3B1FDB31C91 CRC64;

Query Match

3.0%; Score 105; DB 16; Length 523;

Best Local Similarity 22.2%; Pred. No. 4.4;

Matches 105; Conservative 44; Mismatches 143; Indels 182; Gaps 25;

Qy 301 TLRCLPK-----LEAALCQRHDMHTLCKDLP-----NATARES 334
Db 88 TLRALRAYPALLRQKLPASLLWRRFSPTRSFDLPVQLQLEGLAGEPQRSRLVLSQRNAG 147
Qy 335 GWYVLEKVDLHPQLCFKVPWFSEFGNSHVECPHQTGSLTSWNVMDTQAQQLIL---HFS 392
Db 148 GATWLTVVGVHLEMA-----WAGFAMLLYLLIPAQNEIDWNQSLDPEAGEWLWLEHLS 203
Qy 393 SRMHATFSAANSLPCLGQDTLVPVY-----TVSQVWRSVDQFAWKHLLCPDV 440
Db 204 NLLYVLVLVWME-----PIYVACGFTLYLNRRTLEAW---DIELVFRRL----- 245
Qy 441 SYRHIG---LILALLALLTLLGVVLTALTCRRPQSGPGP---ARPVLLHAAADSEAQRRL 494
Db 246 RQRLVGSAYVLLGLTASLAWL-----PAPSAYAEPA-----AATSAGEAEL 287
Qy 495 VGALAEALLRAALG---GGRDV---IVD----- 515
Db 288 PPEQARLLRQKLNSEQAGKQIRAIVDGAPFKNSETVTGWRFQDKTEKKDSRKEDEERLKA 347
Qy 516 LWEG-----RHVARV-GPLPW-----LWAAR-----TRVAREOQT 544
Db 348 FFEALANWVPERHAAQVIEVLLWALLEFSAVFLVWRYREWLRFVGNLGLPQARRREAPT 407
Qy 545 VLLLSGADLRPVSGPDRAAPLLALLHAAAPRPLLLLAY---FSRLC-----AK 590
Db 408 VMF---GLDLSPESLPDDIASNAERLWNEKPREALGLLYRGLLSRLLDYRLPLKGSHT 464
Qy 591 GDIPPLRALPRYRLRLDPLRLRALDARFAEATSWG-RIGARQRQSRLELC 643
Db 465 GEVLRLVEGLEQQRPLLYSOLLTAQ-----WQALAYGHRLPADDTTQ---RLC 510

Search completed: January 28, 2003, 09:30:33

Job time : 50 secs